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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:50:39 ; Search time 16.5 Seconds
(without alignments)
206.504 Million cell updates/sec

Title: US-09-654-743-24
Perfect score: 386
Sequence: 1 YEARIIVFTGWIYSVNKEQL.....KPSDDPDQHAQYPCCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	386	100.0	66	2	US-08-511-485-24
2	386	100.0	66	4	US-09-201-936-24
3	386	100.0	66	4	US-09-011-356-24
4	386	100.0	496	2	US-08-511-485-10
5	386	100.0	496	3	US-09-212-971-10
6	386	100.0	496	3	US-08-800-929A-10
7	386	100.0	496	4	US-09-617-053A-10
8	386	100.0	496	4	US-09-201-936-10
9	386	100.0	496	4	US-09-011-356-10
10	386	100.0	496	4	US-09-672-717-225
11	366	94.8	66	2	US-08-511-485-25
12	366	94.8	66	4	US-09-201-936-25
13	366	94.8	66	4	US-09-011-356-25
14	366	94.8	236	4	US-09-239-867-4
15	366	94.8	497	2	US-08-511-485-4
16	366	94.8	497	3	US-09-212-971-4
17	366	94.8	497	3	US-08-800-929A-4
18	366	94.8	497	4	US-09-617-053A-4
19	366	94.8	497	4	US-08-657-759-2
20	366	94.8	497	4	US-09-201-936-4
21	366	94.8	497	4	US-09-011-356-4
22	366	94.8	497	4	US-09-672-717-219
23	334	86.5	236	3	US-09-121-979-4
24	334	86.5	236	3	US-09-332-319-4
25	334	86.5	236	4	US-09-239-867-2
26	279	72.3	53	4	US-08-657-759-19
27	233	60.4	50	3	US-08-975-080-28

28	233	60.4	50	3	US-08-975-080-29	Sequence 29, Appl
29	233	60.4	50	3	US-08-975-080-32	Sequence 32, Appl
30	198	51.3	68	2	US-08-511-485-26	Sequence 26, Appl
31	198	51.3	68	4	US-09-201-936-26	Sequence 26, Appl
32	198	51.3	68	4	US-09-011-356-26	Sequence 26, Appl
33	198	51.3	604	2	US-08-511-485-6	Sequence 6, Appl
34	198	51.3	604	3	US-09-212-971-6	Sequence 6, Appl
35	198	51.3	604	3	US-08-800-929A-6	Sequence 6, Appl
36	198	51.3	604	3	US-08-569-749-4	Sequence 4, Appl
37	198	51.3	604	4	US-09-617-053A-6	Sequence 6, Appl
38	198	51.3	604	4	US-09-201-936-6	Sequence 6, Appl
39	198	51.3	604	4	US-09-011-356-6	Sequence 6, Appl
40	198	51.3	604	4	US-09-672-717-221	Sequence 221, Appl
41	198	51.3	604	5	PCT-US96-12860-4	Sequence 28, Appl
42	190	49.2	68	2	US-08-511-485-28	Sequence 28, Appl
43	190	49.2	68	4	US-09-201-936-28	Sequence 28, Appl
44	190	49.2	68	4	US-09-011-356-28	Sequence 28, Appl
45	190	49.2	268	3	US-08-836-134-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-511-485-24
; Sequence 24, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/511,485
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/POCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
; US-08-511-485-24

Query Match 100.0%; Score 386; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIIVFTGWIYSVNKEQLAGFYALGSDGVKFCFHCGLTDWKPSPDQHAQY 60
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Db 1 YEARIIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAACY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 2
US-09-201-936-24
; Sequence 24, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-24

Query Match 100.0%; Score 386; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YEARIIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAACY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 3
US-09-011-356-24
; Sequence 24, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; EARLIER FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
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; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-011-356-24

Query Match 100.0%; Score 386; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YEARIIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAACY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 4
US-08-511-485-10
; Sequence 10, Application US/08511485
; Patent No. 591912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
US-08-511-485-10

Query Match 100.0%; Score 386; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.3e-42;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 264 YEARIIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAACY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-800-929A-10
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; Query Match 100.0%; Score 386; DB 3; Length 496;
; Best Local Similarity 100.0%; Pred. No. 3.3e-42;
; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 264 YEARIVTFTGIYVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSSEDPWDQHAICY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 7
US-09-617-053A-10
; Sequence 10, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-617-053A-10
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; Query Match 100.0%; Score 386; DB 4; Length 496;
; Best Local Similarity 100.0%; Pred. No. 3.3e-42;
; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 264 YEARIVTFTGIYVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSSEDPWDQHAICY 323

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-800-929A-10
;
; Query Match 100.0%; Score 386; DB 3; Length 496;
; Best Local Similarity 100.0%; Pred. No. 3.3e-42;
; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 YEARIVTFTGIYVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSSEDPWDQHAICY 60
Db 264 YEARIVTFTGIYVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSSEDPWDQHAICY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 6
US-08-800-929A-10
; Sequence 10, Application US/08800929A
; Patent No. 6133437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-800-929A-10
;
; Query Match 100.0%; Score 386; DB 3; Length 496;
; Best Local Similarity 100.0%; Pred. No. 3.3e-42;
; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 YEARIVTFTGIYVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSSEDPWDQHAICY 60
Db 264 YEARIVTFTGIYVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSSEDPWDQHAICY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 7
US-09-617-053A-10
; Sequence 10, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-617-053A-10
;
; Query Match 100.0%; Score 386; DB 4; Length 496;
; Best Local Similarity 100.0%; Pred. No. 3.3e-42;
; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 YEARIVTFTGIYVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSSEDPWDQHAICY 60
Db 264 YEARIVTFTGIYVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSSEDPWDQHAICY 323

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-800-929A-10
;
; Query Match 100.0%; Score 386; DB 3; Length 496;
; Best Local Similarity 100.0%; Pred. No. 3.3e-42;
; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 YEARIVTFTGIYVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSSEDPWDQHAICY 60
Db 264 YEARIVTFTGIYVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSSEDPWDQHAICY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 6
US-08-800-929A-10
; Sequence 10, Application US/08800929A
; Patent No. 6133437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0

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QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 8
US-09-201-936-10
; Sequence 10, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-10

Query Match 100.0%; Score 386; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.3e-42;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVTGTWIIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPPDQHAKEY 60
Db 264 YEARIVTGTWIIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPPDQHAKEY 323

RESULT 9
US-09-011-356-10
; Sequence 10, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003002
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-011-356-10

Query Match 100.0%; Score 386; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.3e-42;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVTGTWIIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPPDQHAKEY 60
Db 264 YEARIVTGTWIIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPPDQHAKEY 323

RESULT 10
US-09-672-717-225
; Sequence 225, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Lacasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; FILE REFERENCE: 07891/025001
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-672-717-225

Query Match 100.0%; Score 386; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.3e-42;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVTGTWIIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPPDQHAKEY 60
Db 264 YEARIVTGTWIIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPPDQHAKEY 323

RESULT 11
US-08-511-485-25
; Sequence 25, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```


COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-25

Query Match 94.8%; Score 366; DB 2; Length 66;
Best Local Similarity 95.5%; Pred. No. 1.2e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDWDQAKCY 60
DB 1 YEARIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDWDQAKCY 60

QY 61 PGCKYL 66
DB 61 PGCKYL 66

RESULT 12
US-09-201-936-25
Sequence 25, Application US/09201936
Patent No. 6541457
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 25
LENGTH: 66
TYPE: PRT
ORGANISM: Homo sapiens
US-09-201-936-25

Query Match 94.8%; Score 366; DB 4; Length 66;
Best Local Similarity 95.5%; Pred. No. 1.2e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDWDQAKCY 60

DB 1 YEARIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDWDQAKCY 60
QY 61 PGCKYL 66
DB 61 PGCKYL 66

RESULT 13

US-09-011-356-25
Sequence 25, Application US/09011356A
Patent No. 6656704
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
FILE REFERENCE: 07891/003002
CURRENT APPLICATION NUMBER: US/09/011,356A
CURRENT FILING DATE: 1998-09-14
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 66
TYPE: PRT
ORGANISM: Homo sapiens
US-09-011-356-25

Query Match 94.8%; Score 366; DB 4; Length 66;
Best Local Similarity 95.5%; Pred. No. 1.2e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDWDQAKCY 60
DB 1 YEARIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDWDQAKCY 60

QY 61 PGCKYL 66
DB 61 PGCKYL 66

RESULT 14
US-09-239-867-4
Sequence 4, Application US/09239867
Patent No. 6331412
GENERAL INFORMATION:
APPLICANT: Robert G. Korneluk et al.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
FILE REFERENCE: 07891/018002
CURRENT APPLICATION NUMBER: US/09/239,867
CURRENT FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/073,001
PRIOR FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 236
TYPE: PRT
ORGANISM: Homo sapiens
US-09-239-867-4

Query Match 94.8%; Score 366; DB 4; Length 236;
Best Local Similarity 95.5%; Pred. No. 5.6e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARTVFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWQHAKCY 60
 Db 4 YEARTVFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWQHAKCY 63
 QY 61 PGCKYL 66
 Db 64 PGCKYL 69

RESULT 15

US-08-511-485-4
 ; Sequence 4, Application US/08511485
 ; Patent No. 5919912
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Baird, Stephen
 ; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/511,485
 ; FILING DATE: 04-AUG-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul T.
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 07540/002001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617/542-5070
 ; TELEFAX: 617/542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 497 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: both
 ; MOLECULE TYPE: protein
 ; US-08-511-485-4

Query Match 94.8%; Score 366; DB 2; Length 497;
 Best Local Similarity 95.5%; Pred. No. 1.4e-39;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YEARTVFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWQHAKCY 60
 Db 265 YEARTVFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWQHAKCY 324
 QY 61 PGCKYL 66
 Db 325 PGCKYL 330

Search completed: March 10, 2004, 13:55:49
 Job time : 17.5 secs

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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:42:09 ; Search time 49.5 Seconds

(without alignments)
376.730 Million cell updates/sec

Title: US-09-654-743-24

Perfect score: 386

Sequence: 1 YEARIVTFGTWISYVNKEQL.....KFSEDPWDQAKYFGCKYL 66

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04:*

- 1: GeneseqP1980s:*
- 2: GeneseqP1980s:*
- 3: GeneseqP2000s:*
- 4: GeneseqP2001s:*
- 5: GeneseqP2002s:*
- 6: GeneseqP2003as:*
- 7: GeneseqP2003bs:*
- 8: GeneseqP2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	386	100.0	496	2	AAW19584 Mouse apo
2	386	100.0	496	2	AAW69297 Murine XI
3	386	100.0	496	5	ABG65666 Mouse inh
4	372	96.4	66	7	ADB61828 Mouse inh
5	372	96.4	496	6	ABP72157 Mouse inh
6	366	94.8	66	7	ADB61827 Rat inhib
7	366	94.8	66	7	ADB61810 Human inh
8	366	94.8	236	5	ABG32418 X-linked
9	366	94.8	278	5	AAO20511 Protein o
10	366	94.8	497	2	AAW19581 Human apo
11	366	94.8	497	2	AAW69294 Human XIA
12	366	94.8	497	3	AAW59451 Human XIA
13	366	94.8	497	3	AAW99985 Human X-1
14	366	94.8	497	5	ABG65663 Human inh
15	366	94.8	497	7	ADB80961 RING-SH c
16	357	92.5	496	2	AAW19745 Mouse inh
17	334	86.5	66	7	ADB61820 Human inh
18	334	86.5	236	3	AAW81440 Human TIA
19	334	86.5	236	4	AAE00365 Human IAP
20	334	86.5	236	5	AAU75066 Human tes
21	334	86.5	236	5	ABG32417 Inhibitor
22	334	86.5	464	5	AAU75747 Human inh
23	328	85.0	236	4	AAE00366 Chimpanze
24	325	84.2	66	7	ADB61831 Gorilla i
25	325	84.2	236	4	AAE00367 Gorilla I

26	306	79.3	57	7	ADB61832 Unidentif
27	279	72.3	66	7	ADB61829 Chicken i
28	258	66.8	52	7	ADB61830 Bovine inh
29	212	54.9	68	7	ADB61833 Zebra fis
30	198	51.3	68	7	ADB61813 Human inh
31	198	51.3	557	6	ABP72159 Inhibitor
32	198	51.3	604	2	AAW19582 Human apo
33	198	51.3	604	2	AAW19747 Human inh
34	198	51.3	604	2	AAW13546 Human c-I
35	198	51.3	604	2	AAW69295 Human HIA
36	198	51.3	604	2	AAW52703 Human cel
37	198	51.3	604	2	AAW33997 Human cel
38	198	51.3	604	5	ABG65664 Human inh
39	198	51.3	604	6	ABU07431 Protein d
40	198	51.3	604	6	ABW82739 Human CIA
41	198	51.3	604	7	ADB80948 RING-SH c
42	198	51.3	604	7	AAE39811 Human cel
43	198	51.3	1140	5	AAU97837 Human cys
44	198	51.3	1141	4	AAW50594 Human API
45	199	49.0	600	2	AAW69298 Murine HI

ALIGNMENTS

RESULT 1

AAW19584
ID AAW19584 standard; protein; 496 AA.

XX AC AAW19584;

XX AC

DT 02-SEP-1997 (first entry)

XX Mouse apoptosis inhibitor M-XIAP.

DE Mouse apoptosis inhibitor M-XIAP.

XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; M-XIAP;

KW HIV; AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia;

KW myocardial infarction; stroke; reperfusion injury;

KW toxin-induced liver disease; gene therapy; diagnosis.

XX Mus sp.

XX

Key Location/Qualifiers

FT Domain 26..93

FT Domain /label= BIR-1

FT Domain 163..230

FT Domain /label= BIR-2

FT Domain 264..329

FT Domain /label= BIR-3

FT Domain 438..483

FT Domain /label= Ring_zinc_finger

MO9706255-A2..

20-FEB-1997.

05-AUG-1996; 96WO-IB001022.

04-AUG-1995; 95US-00511485.

22-DEC-1995; 95US-00576956.

(UYOT-) UNIV OTTAWA.

Korneluk RG, Mackenzie AE, Baird S, Liston P;

WPI; 1997-154262/14.

N-PSDB; AAT70839.

Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to

inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of

susceptibility to apoptotic disease.

Claim 27; Page 79-80; 219pp; English.

XX Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2
CC (AAW19581-86) are a new class of mammalian proteins that are inhibitors
CC of apoptosis (IAP), and which are characterised by the presence of a zinc
CC finger domain (see also AAW19587) and at least one BIR (baculovirus
CC IAP repeat) domain (see also AAW19588). The M-XIAP amino acid sequence
CC was deduced from the m-xiap gene (AA170839) isolated from a mouse embryo
CC cDNA library. The IAP oligopeptides can be expressed in host cells (in
CC vitro or in vivo) and used in methods for treating diseases and disorders
CC involving apoptosis, esp. in a human diagnosed as HIV-positive or as
CC having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or
CC an ischaemic injury, selected from myocardial infarction, stroke,
CC reperfusion injury, or a toxin-induced liver disease
XX
XX Sequence 496 AA;
SQ
Query Match 100.0%; Score 386; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.5e-39; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEARIIVTGTWYISVKNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPDQHKACY 60
DB 264 YEARIIVTGTWYISVKNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPDQHKACY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329
RESULT 2
AAW69297
ID AAW69297 standard; protein; 496 AA.
XX
AC AAW69297;
XX
DT 13-NOV-1998 (first entry)
XX
DE Murine XIAP protein.
XX
KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KW proliferative disease; IAP; therapy; cancer; mouse; XIAP protein.
XX
OS Mus sp.
XX
PN WO9835693-A2.
XX
PD 20-AUG-1998.
XX
PF 13-FEB-1998; 98WO-IB000781.
XX
PR 13-FEB-1997; 97US-00800929.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Korneluk R, Mackenzie AE, Liston P, Baird S, Tsang B, Pratt C;
XX WPI; 1998-467164/40.
XX
DR N-PSDB; AAV55041.
XX
PT Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
PT or NAIP polypeptide. also methods for prognosis based on presence of IAP
PT and NAIP, specifically applied to cancers involving p53 mutations.
XX
PS Disclosure; Fig 4; 147pp; English.
XX
CC This sequence is the murine XIAP protein, which is an inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver nasopharynx, thyroid, central nervous system, prostate, colon,

CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors
XX
SQ Sequence 496 AA;
Query Match 100.0%; Score 386; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.5e-39; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEARIIVTGTWYISVKNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPDQHKACY 60
DB 264 YEARIIVTGTWYISVKNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPDQHKACY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329
RESULT 3
ABG65666
ID ABG65666 standard; protein; 496 AA.
XX
AC ABG65666;
XX
DT 26-AUG-2002 (first entry)
XX
DE Mouse inhibitor of apoptosis, XIAP.
XX
KW Mouse; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic;
KW cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer;
KW embryonic development; viral pathogenesis; autoimmune disorder;
KW neurodegenerative disease; multiple sclerosis; lupus erythematosus;
KW herpes virus infection; pox virus infection; adenovirus infection;
KW proliferative disease.
XX
OS Mus sp.
XX
PN WO200226968-A2.
XX
PD 04-APR-2002.
XX
PF 27-SEP-2001; 2001WO-CA001379.
XX
PR 28-SEP-2000; 2000US-00672717.
XX
PA (UYOT-) UNIV OTTAWA.
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
PI Korneluk R, Lacasse E, Baird S, Holcik M, Young S;
XX WPI; 2002-479662/51.
XX
DR N-PSDB; ABK93872.
XX
PT Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
PT apoptosis in a cell, for treating cancer and other proliferative
PT diseases.
XX
PS Example 12; Fig 4; 135pp; English.
XX
CC The invention relates to an inhibitor of apoptosis (IAP) antisense of
CC nucleic acid (I) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse or
CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC mammal diagnosed with a proliferative disease. The method is useful for

CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a mouse IAP
 CC protein sequence
 CC
 XX Sequence 496 AA;
 SQ
 Query Match 100.0%; Score 386; DB 5; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1.5e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEARIVTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAACY 60
 DB 264 YEARIVTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAACY 323
 QY 61 PGCKYL 66
 DB 324 PGCKYL 329
 RESULT 4
 AD861828
 ID ADB61828 standard; protein; 66 AA.
 AC
 AC ADB61828;
 DT 04-DEC-2003 (first entry)
 XX
 XX Mouse inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
 XX
 XX baculovirus inhibitor of apoptosis repeat domain; BIR domain;
 KW apoptosis pathway; embryonic development; viral pathogenesis; cancer;
 KW autoimmune disorder; neurodegenerative disease; apoptotic response;
 KW systemic lupus erythematosus; multiple sclerosis; viral infection;
 KW herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
 KW HIAP1; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
 KW caspase-9; cytostatic; neoplasia; leukaemia; colon carcinoma;
 KW cervical cancer; uterine cancer; testicular cancer;
 KW small cell lung carcinoma; uterine cancer; renal cell carcinoma;
 KW Wilm's tumour; BIR 3 domain; mouse; murine.
 XX
 OS Mus sp.
 XX
 XX WO2003040172-A2.
 XX
 XX 15-MAY-2003.
 XX
 XX 12-NOV-2002; 2002WO-CA001738.
 XX
 XX 09-NOV-2001; 2001US-0332300P.
 XX
 XX 08-APR-2002; 2002US-0370934P.
 XX
 XX (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 XX Boudreault A, Korneluk RG, La Casse E, Liston P;
 XX WPI; 2003-513532/48.
 XX
 XX Polypeptide capable of forming a complex with a polypeptide comprising a
 PT baculovirus inhibitor of apoptosis repeat domain useful for treating
 PT cancer and other neoplasms.
 XX
 XX Disclosure; Fig 1B; 53pp; English.
 XX
 XX This invention relates to a substantially pure polypeptide having a
 CC length of less than 100 amino acids and capable of forming a complex with
 CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
 CC (BIR) domain. The apoptosis pathway is known to play a critical role in

CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
 CC and neurodegenerative diseases. The failure of the apoptotic response has
 CC been implicated in the development of cancer, autoimmune disorders (for
 CC example systemic lupus erythematosus and multiple sclerosis) and viral
 CC infections (including herpes virus, poxvirus and adenovirus). The
 CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
 CC (CIAP2) and HIAP2 (CIAP1) all possess three BIR domains and carboxy
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC which inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC may be useful for the treatment of cancer and other neoplasms, such as
 CC leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
 CC and Wilm's tumour, and for enhancing apoptosis. The present sequence is
 CC that of the mouse inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
 CC which was used to demonstrate homology to human IAP protein BIR domains
 CC to which the peptides of the invention are targeted to bind.
 XX
 XX Sequence 66 AA;
 SQ
 Query Match 96.4%; Score 372; DB 7; Length 66;
 Best Local Similarity 97.0%; Pred. No. 8.4e-39;
 Matches 64; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YEARIVTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAACY 60
 DB 1 YEARIVTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAACY 60
 QY 61 PGCKYL 66
 DB 61 PGCKYL 66
 RESULT 5
 ABP72157
 ID ABP72157 standard; protein; 496 AA.
 XX
 XX AC ABP72157;
 XX
 XX 22-APR-2003 (first entry)
 DT
 DE Mouse inhibitor of apoptosis protein MIAP3.
 DE
 DE Inhibitor of apoptosis; MIAP3; mouse; apoptosis; cancer; leukaemia;
 KW lymphoma; neuroblastoma; carcinoma; melanoma; cytostatic; gene therapy.
 XX
 XX Mus sp.
 XX
 XX WO2003004606-A2.
 XX
 XX 16-JAN-2003.
 XX
 XX 03-JUL-2002; 2002WO-US021002.
 XX
 XX 03-JUL-2001; 2001US-00898158.
 XX
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 XX Troy CM, Shelanski ML;
 XX WPI; 2003-210351/20.
 DR N-PSDB; ABZ58102.
 XX
 XX New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for
 PT treating cancer, neurodegenerative disorder or cardiomyopathy.
 XX
 XX Disclosure; Fig 15A; 124pp; English.
 XX
 XX The present sequence is the protein sequence of murine inhibitor of
 CC apoptosis protein MIAP3. The invention provides a nucleic acid, such as

CC an antisense oligonucleotide, which specifically hybridises to a nucleic
 CC acid encoding an inhibitor of apoptosis protein, especially XIAP1, XIAP2,
 CC MIAP3, CIAP1, CIAP2 and XIAP. A claimed method for inducing a cell's
 CC death comprises contacting the cell with the nucleic acid under
 CC conditions permitting the nucleic acid to enter the cell, especially the
 CC use of a vector, liposome, or a mechanical or electrical means. The
 CC method is used to treat acute lymphocytic leukaemia, acute myelogenous
 CC leukaemia, lung cancer, breast cancer, ovarian cancer, prostate cancer,
 CC lymphoma, Hodgkin's disease, malignant melanoma, neuroblastoma, renal
 CC cell carcinoma and squamous cell carcinoma (all claimed)

XX Sequence 496 AA;

Query Match 96.4%; Score 372; DB 6; Length 496;
 Best Local Similarity 97.0%; Pred. No. 8.8e-38;
 Matches 64; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDWDQAKCY 60
 DB 264 YEARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDWDQAKCY 323

QY 61 PGCKYL 66

DB 324 PGCKYL 329

RESULT 6

ID ADB61827 standard; protein; 66 AA.

XX ADB61827;

DT 04-DEC-2003 (first entry)

DE Rat inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.

XX baculovirus inhibitor of apoptosis repeat domain; BIR domain;
 KW apoptosis pathway; embryonic development; viral pathogenesis; cancer;
 KW autoimmune disorder; neurodegenerative disease; apoptotic response;
 KW systemic lupus erythematosus; multiple sclerosis; viral infection;
 KW herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
 KW HIAP1; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
 KW caspase-9; cytosolic; neoplasm; leukaemia; colon carcinoma;
 KW cervical cancer; uterine cancer; testicular cancer;
 KW small cell lung carcinoma; rat.
 XX Wilm's tumour; BIR 3 domain; rat.

XX Rattus sp.

XX WO2003040172-A2.

XX 15-MAY-2003.

XX 12-NOV-2002; 2002WO-CA001738.

XX 09-NOV-2001; 2001US-0332300P.

XX 08-APR-2002; 2002US-0370934P.

XX (AEGE-) AEGERA THERAPEUTICS INC.

XX Boudreault A, Korneluk RG, La Casse E, Liston P;

XX WPI; 2003-513532/48.

XX Polypeptide capable of forming a complex with a polypeptide comprising a
 PT baculovirus inhibitor of apoptosis repeat domain useful for treating
 PT cancer and other neoplasms.

XX Disclosure; Fig 1B; 53pp; English.

XX This invention relates to a substantially pure polypeptide having a
 CC length of less than 100 amino acids and capable of forming a complex with
 CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat

CC (BIR) domain. The apoptosis pathway is known to play a critical role in
 CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
 CC and neurodegenerative diseases. The failure of the apoptotic response has
 CC been implicated in the development of cancer, autoimmune disorders (for
 CC example systemic lupus erythematosus and multiple sclerosis) and viral
 CC infections (including herpes virus, poxvirus and adenovirus). The
 CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
 CC (CIAP2) and HIAP2 (CIAP1) all possess three BIR domains and carboxy
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC which inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC are useful for the treatment of cancer and other neoplasms, such as
 CC leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
 CC and Wilm's tumour, and for enhancing apoptosis. The present sequence is
 CC that of the rat inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
 CC which was used to demonstrate homology to human IAP protein BIR domains
 CC to which the peptides of the invention are targeted to bind.

XX Sequence 66 AA;

Query Match 94.8%; Score 366; DB 7; Length 66;

Best Local Similarity 93.9%; Pred. No. 4.7e-38;

Matches 62; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDWDQAKCY 60
 DB 1 YDARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDWDQAKWY 60

QY 61 PGCKYL 66

DB 61 PGCKYL 66

RESULT 7

ADB61810

ID ADB61810 standard; protein; 66 AA.

XX ADB61810;

DT 04-DEC-2003 (first entry)

DE Human inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.

XX baculovirus inhibitor of apoptosis repeat domain; BIR domain;
 KW apoptosis pathway; embryonic development; viral pathogenesis; cancer;
 KW autoimmune disorder; neurodegenerative disease; apoptotic response;
 KW systemic lupus erythematosus; multiple sclerosis; viral infection;
 KW herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
 KW HIAP1; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
 KW caspase-9; cytosolic; neoplasm; leukaemia; colon carcinoma;
 KW cervical cancer; uterine cancer; testicular cancer;
 KW small cell lung carcinoma; rat.
 XX Wilm's tumour; human; BIR 3 domain.

XX Homo sapiens.

XX WO2003040172-A2.

XX 15-MAY-2003.

XX 12-NOV-2002; 2002WO-CA001738.

XX 09-NOV-2001; 2001US-0332300P.

XX 08-APR-2002; 2002US-0370934P.

XX (AEGE-) AEGERA THERAPEUTICS INC.

XX Boudreault A, Korneluk RG, La Casse E, Liston P;

DR WPI; 2003-513532/48.
 XX
 PT Polypeptide capable of forming a complex with a polypeptide comprising a
 PT baculovirus inhibitor of apoptosis repeat domain useful for treating
 PT cancer and other neoplasms.
 XX
 PS Disclosure; Fig 1A; 53pp; English.
 XX
 CC This invention relates to a substantially pure polypeptide having a
 CC length of less than 100 amino acids and capable of forming a complex with
 CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
 CC (BIR) domain. The apoptosis pathway is known to play a critical role in
 CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
 CC and neurodegenerative diseases. The failure of the apoptotic response has
 CC been implicated in the development of cancer, autoimmune disorders (for
 CC example systemic lupus erythematosus and multiple sclerosis) and viral
 CC infections (including herpes virus, poxvirus and adenovirus. The
 CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
 CC (CIAP2) and HIAP2 (CIAP1) all possess three BIR domains and carboxy
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC which inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC may be useful for the treatment of cancer and other neoplasms, such as
 CC leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
 CC and Wilms' tumour, and for enhancing apoptosis. The present sequence is
 CC that of the human inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
 CC against which the peptides of the invention are targeted to bind.
 XX
 SQ Sequence 66 AA;
 Query Match 94.8%; Score 366; DB 7; Length 66;
 Best Local Similarity 95.5%; Pred. No. 4.7e-36;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YEARIVTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPDQHAQKY 60
 DB 1 YEARIFTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPDQHAQKY 60
 QY 61 PGCKYL 66
 DB 61 PGCKYL 66
 RESULT 8
 AEG32418
 ID AEG32418 standard; protein; 236 AA.
 XX
 AC AEG32418;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE X-linked inhibitor of apoptosis protein, XIAP.
 XX
 KW Inhibitor of apoptosis protein; IAP; testis; TIAP; apoptosis; inhibitor;
 KW fertility; testicular cancer; male infertility; male birth control;
 KW X-linked inhibitor of apoptosis protein; XIAP.
 XX
 OS Mammalia.
 XX
 FT Key Location/Qualifiers
 FT Misc-difference 1
 FT /note= "Encoded by nnn; start codon is illegible in
 FT specification"
 FT
 FT US2002086409-A1.
 PN
 XX 04-JUL-2002.
 XX
 PD 18-DEC-2001; 2001US-00024433.
 PF

XX 29-JAN-1998; 98US-0073001P.
 PR 29-JAN-1999; 99US-00239867.
 XX
 PA (KORN/) KORNELUK R G.
 PA (LAGA/) LAGACE M.
 XX
 PI Korneluk RG, Lagace M;
 XX
 DR WPI; 2002-642245/69.
 DR N-PSDB; ABS52803.
 XX
 PT Novel polypeptide, a member of inhibitor of apoptosis family of proteins
 PT that is expressed in testes useful for modulating apoptosis in cells,
 PT particular cells involved in male fertility.
 XX
 PS Example 3; Fig 4B; 24pp; English.
 XX
 CC A substantially pure TIAP polypeptide (I), a member of IAP (inhibitor of
 CC apoptosis) family of proteins that is expressed in the testes. (I) is
 CC useful for identifying a compound that modulates TIAP biological activity
 CC (I) is useful for increasing fertility in a cell, preferably a germ-line
 CC cell and for increasing fertility in an animal. (I) is useful for
 CC treating or preventing apoptosis which occurs as a part of testicular
 CC cancer and male infertility. TIAP may be manipulated for use as a male
 CC birth control. TIAP polypeptides and nucleic acid sequences also have
 CC diagnostic use in the detection or monitoring of conditions involving
 CC aberrant levels of apoptosis. The present sequence represents the amino
 CC acid sequence of X-linked inhibitor of apoptosis protein, XIAP
 XX
 SQ Sequence 236 AA;
 Query Match 94.8%; Score 366; DB 5; Length 236;
 Best Local Similarity 95.5%; Pred. No. 2.1e-37;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YEARIVTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPDQHAQKY 60
 DB 4 YEARIFTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPDQHAQKY 63
 QY 61 PGCKYL 66
 DB 64 PGCKYL 69
 RESULT 9
 AAO20511
 ID AAO20511 standard; protein; 278 AA.
 XX
 AC AAO20511;
 XX
 DT 27-JUN-2002 (first entry)
 XX
 DE Protein of APP related human homologue hCP35211.
 XX
 KW Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta;
 KW amyloid precursor protein; tissue-specific expression control; human APP;
 KW APP pathway modulator; Gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200226820-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 01-OCT-2001; 2001WO-EP011345.
 XX
 PR 29-SEP-2000; 2000US-0236893P.
 PR 14-JUN-2001; 2001US-0298309P.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX

PI Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;
 PI Reinhardt MHEW, Zusman S;
 DR WPI; 2002-315796/35.
 DR N-PSDB; AAK99405.

XX New transgenic fly, containing DNA encoding an Abeta portion of human
 PT APP, useful for identifying agents which modulate the APP pathway and
 PT which can be used to treat Alzheimer's disease.

XX Example 4; Page 112; 129pp; English.

XX The invention relates to a transgenic fly whose genome comprises DNA
 CC encoding a polypeptide having the Abeta portion of human amyloid
 CC precursor protein (APP), fused to a signal sequence. The DNA sequence
 CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
 CC the specification. The DNA sequence is operably linked to a tissue-
 CC specific expression control sequence. Expression of the sequence gives
 CC the fly an altered phenotype. The purpose of the invention is for
 CC identifying agents that inhibit or promote the expression and/or function
 CC of genes or encoded polypeptides which modify the APP pathway. The agent
 CC is a compound, triple helix DNA, antisense oligonucleotide, double
 CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used
 CC to treat conditions such as Alzheimer's disease. The agent can be used as
 CC an APP pathway modulator or in gene therapy. This sequence represents the
 CC protein of the APP related human homologue hCP35211

XX Sequence 278 AA;

Query Match 94.8%; Score 366; DB 5; Length 278;
 Best Local Similarity 95.5%; Pred. No. 2.5e-37;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPPWDQAKCY 60
 DB 46 YEARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPPWDQAKCY 105
 QY 61 PGCKYL 66
 DB 106 PGCKYL 111

RESULT 10

AAW19581
 ID AAW19581 standard; protein; 497 AA.

AC AAW19581;

DT 02-SRP-1997 (first entry)

DE Human apoptosis inhibitor XIAP.

XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; XIAP; HIV;
 XX AIDS; neurodegeneration; myelodysplastic syndrome; leukaemia;
 XX myocardial infarction; stroke; reperfusion injury;
 XX toxin-induced liver disease; gene therapy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Domain 25..93
 FT /label= BIR-1
 FT Domain 163..230
 FT /label= BIR-2
 FT Domain 265..330
 FT /label= BIR-3
 FT Domain 439..484
 FT /label= Ring_zinc_finger

XX WO9706255-A2.

XX 20-FEB-1997.

PF 05-AUG-1996; 96WO-IB001022.
 XX
 PR 04-AUG-1995; 95US-00511485.
 PR 22-DEC-1995; 95US-00576936.
 XX
 XX (UYOT-) UNIV OTTAWA.

XX Korneluk RG, Mackenzie AE, Baird S, Liston P;
 XX WPI; 1997-154262/14.
 DR N-PSDB; AAT70836.

XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
 PT inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of
 PT susceptibility to apoptotic disease.

XX Claim 27; Page 68-70; 219pp; English.

XX Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2
 CC (AAW19581-86) are a new class of mammalian proteins that are inhibitors
 CC of apoptosis (IAP) and which are characterised by the presence of a ring
 CC zinc finger domain (see also AAW19587) and at least one BIR (baculovirus
 CC IAP repeat) domain (see also AAW19588). The XIAP amino acid sequence was
 CC deduced from the xiap gene (AAT70836) isolated from a human foetal brain
 CC cDNA library. IAP polypeptides can be expressed in host cells (in vitro
 CC or in vivo) and used in methods for treating diseases and disorders
 CC involving apoptosis, esp. in a human diagnosed as HIV-positive or as
 CC having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or
 CC an ischaemic injury, selected from myocardial infarction, stroke,
 CC reperfusion injury, or a toxin-induced liver disease

XX Sequence 497 AA;

Query Match 94.8%; Score 366; DB 2; Length 497;

Best Local Similarity 95.5%; Pred. No. 5e-37;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPPWDQAKCY 60
 DB 265 YEARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPPWDQAKCY 324
 QY 61 PGCKYL 66
 DB 325 PGCKYL 330

RESULT 11

AAW69294
 ID AAW69294 standard; protein; 497 AA.

AC AAW69294;

DT 13-NOV-1998 (first entry)

XX Human XIAP protein.

XX Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
 XX proliferative disease; IAP; therapy; cancer; human; XIAP protein.

XX Homo sapiens.

XX WO9835693-A2.

XX 20-AUG-1998.

XX 13-FEB-1998; 98WO-IB000781.

XX 13-FEB-1997; 97US-00800929.

XX (UYOT-) UNIV OTTAWA.

XX Korneluk R, Mackenzie AE, Liston P, Baird S, Tsang B, Pratt C;

DR WPI; 1998-467164/40.
DR N-PSDB; AAV55038.

PT Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
PT or NAIP polypeptide - also methods for prognosis based on presence of IAP
PT and NAIP, specifically applied to cancers involving p53 mutations.

XX Disclosure; Fig 1; 147pp; English.

XX This sequence is the human XIAP protein, which is an inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis.
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors

XX Sequence 497 AA;

Query Match 94.8%; Score 366; DB 2; Length 497;

Best Local Similarity 95.5%; Pred. No. 5e-37; Indels 0; Gaps 0;
Matches 63; Conservative 1; Mismatches 2;

QY 1 YEARIVTFTWYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAQKY 60
DB 265 YEARIVTFTWYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAQKY 324

QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 12

AA59451
ID AAY59451 standard; protein; 497 AA.

XX AAY59451;

XX 24-MAR-2000 (first entry)

XX Human XIAP protein sequence.

XX Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
KW transforming growth factor-beta activated kinase 1; monocyte migration;
KW TAK1 binding protein 1; extracellular matrix protein production;
KW cell growth inhibitor; beta-amyloid protein deposition;
KW immunosuppression; Transforming growth factor-beta.

XX Homo sapiens.

XX JP11326328-A.

XX 26-NOV-1999.

XX 13-MAY-1998; 98JP-00130378.

XX 13-MAY-1998; 98JP-00130378.

XX (MATS/) MATSUMOTO K.

XX WPI; 2000-078337/07.

XX N-PSDB; AAZ48862.

XX Screening a substance which inhibits combination of the X-linked
PT inhibitor of apoptosis protein.

XX

PS Claim 3; Page 28-30; 43pp; Japanese.

XX This sequence represents the human XIAP protein. The invention relates to
CC a method for screening a substance inhibiting the formation of a complex
CC between XIAP and TAB1, in which X-linked inhibitor of apoptosis protein
CC (XIAP), transforming growth factor-beta activated kinase 1 (TAK1) binding
CC protein 1 (TAB1) and a substance to be tested are contacted with each
CC other and then the presence or formation of a complex between XIAP and
CC TAB1 is detected. The substance can be used as a drug for extracellular
CC matrix protein production enhancement, cell growth inhibition, monocyte
CC migration, physiologically active substance induction, immunosuppression,
CC and beta-amyloid protein deposition. A substance inhibiting the formation
CC of a complex between TAB1 and XIAP as well as between XIAP and TGF-beta
CC (transforming growth factor-beta) type I and/or type II receptor is
CC useful as a drug

XX Sequence 497 AA;

Query Match 94.8%; Score 366; DB 3; Length 497;

Best Local Similarity 95.5%; Pred. No. 5e-37; Indels 0; Gaps 0;
Matches 63; Conservative 1; Mismatches 2;

QY 1 YEARIVTFTWYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAQKY 60
DB 265 YEARIVTFTWYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAQKY 324

QY 61 PGCKYL 66

DB 325 PGCKYL 330

RESULT 13

AA59985
ID AAY99985 standard; protein; 497 AA.

XX AAY99985;

XX 07-NOV-2000 (first entry)

XX Human X-linked inhibitor of apoptosis.

XX X-linked inhibitor of apoptosis; XIAP; hILP; MIHA; U45880; antisense;
KW antiinflammatory; cytostatic; tumour.

XX Homo sapiens.

XX US6087173-A.

XX 11-JUL-2000.

XX 09-SEP-1999; 99US-00392580.

XX 09-SEP-1999; 99US-00392580.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Cowser LM, Ackermann EJ;

XX WPI; 2000-498201/44.

XX N-PSDB; AAA64901.

XX Antisense compound useful for research reagents, diagnostics, prophylaxis
PT and for treating disorders associated with X-linked inhibitor of
PT apoptosis, modulates expression of X-linked inhibitor of apoptosis.

XX Example 13; Col 43-48; 33pp; English.

XX The present invention relates to antisense oligonucleotides designed to
CC inhibit expression of the human X-linked inhibitor of apoptosis (the
CC present sequence). Modified phosphorothioate 2'-MOE oligonucleotides are
CC more effective inhibitors than unmodified oligonucleotides. The
CC oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis

CC expression in cells and tissues in vitro. The oligonucleotides are also
 CC useful for treating animals or humans, prone to a disease associated with
 CC X-linked inhibitor of apoptosis. The oligonucleotides may also be used
 CC prophylactically to prevent infection, inflammation or tumour formation
 XX
 SQ Sequence 497 AA;

Query Match 94.8%; Score 366; DB 3; Length 497;
 Best Local Similarity 95.5%; Pred. No. 5e-37;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YEARIYFTGTWYVSNKQLARAGFYALGEGDKVKCFHCGGLTDMKPSDPMQDQAKY 60
 DB 265 YEARIYFTGTWYVSNKQLARAGFYALGEGDKVKCFHCGGLTDMKPSDPMQDQAKY 324
 QY 61 PGCKYL 66
 DB 325 PGCKYL 330

RESULT 14
 ABG65663
 ID ABG65663 standard; protein; 497 AA.

XX AC ABG65663;
 XX DT 26-AUG-2002 (first entry)
 XX DE Human inhibitor of apoptosis, XIAP.
 XX KW Human; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic;
 XX KW cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer;
 XX KW embryonic development; viral pathogenesis; autoimmune disorder;
 XX KW neurodegenerative disease; multiple sclerosis; lupus erythematosus;
 XX KW herpes virus infection; pox virus infection; adenovirus infection;
 XX KW proliferative disease.

XX OS Homo sapiens.
 XX PN WO200226968-A2.
 XX PD 04-APR-2002.
 XX PF 27-SEP-2001; 2001WO-CA001379.
 XX PR 28-SEP-2000; 2000US-00672717.
 XX PA (UYOT-) UNIV OTTAWA.
 XX PA (AEGE-) AEGERA THERAPEUTICS INC.

XX PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
 XX DR WPI; 2002-479562/51.
 XX DR N-PSDB; ABX93869.

XX Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
 PT apoptosis in a cell, for treating cancer and other proliferative
 PT diseases.

XX Example 12; Fig 1; 135pp; English.

XX The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse or
 CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,

CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a human IAP
 CC protein sequence
 XX

SQ Sequence 497 AA;
 Query Match 94.8%; Score 366; DB 5; Length 497;
 Best Local Similarity 95.5%; Pred. No. 5e-37;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YEARIYFTGTWYVSNKQLARAGFYALGEGDKVKCFHCGGLTDMKPSDPMQDQAKY 60
 DB 265 YEARIYFTGTWYVSNKQLARAGFYALGEGDKVKCFHCGGLTDMKPSDPMQDQAKY 324
 QY 61 PGCKYL 66
 DB 325 PGCKYL 330

RESULT 15
 ADB80961

ID ADB80961 standard; protein; 497 AA.

XX AC ADB80961;
 XX DT 04-DEC-2003 (first entry)
 XX DE RING-SH complex related protein, SEQ ID No 35.
 XX KW RING-SH 3; Gag protein; Gag late domain; PI3K; actin; myosin; Hsp60;
 XX KW Hsp70; Hsp90; STAM1; STAM2A; STAM2B; VHS-UTM; GTPase; E2 enzyme; tsGI01;
 XX KW cullin; RING-SH; clathrin; virucide; vaccine; antiviral; retrovirus;
 XX KW rhadovirus; filovirus.

XX OS Unidentified.

XX PN WO2003033646-A2.

XX PD 24-APR-2003.

XX PF 31-JUL-2002; 2002WO-US024589.

XX PR 31-JUL-2001; 2001US-0308958P.

XX PR 09-NOV-2001; 2001US-0345846P.

XX PA (PROT-) PROTEOLOGICS INC.

XX PI Greener T, Moskowitz H, Reiss V, Alroy I;

XX DR WPI; 2003-393509/37.

XX DR N-PSDB; ADB81002.

XX New isolated protein complex comprising a RING-SH 3 polypeptide and
 PT another polypeptide, useful for detecting cells infected with a virus,
 PT and for treating vital disorders caused by retroviruses, rhadoviruses,
 PT or filoviruses.

XX Disclosure; Fig 35; 176pp; English.

XX The invention relates to a novel isolated protein complex comprising a
 CC RING-SH 3 polypeptide and a polypeptide selected from a Gag protein, a
 CC Gag late domain, PI3K, actin, myosin, Hsp60, Hsp70, Hsp90, STAM1, STAM2A,
 CC STAM2B, VHS-UTM, a GTPase, an E2 enzyme, tsGI01, a cullin, RING-SH, and a
 CC clathrin. The novel protein complex has virucide activity and can be used
 CC to treat disorders as part of a vaccine. The protein complex and
 CC composition are useful for detecting cells infected with a virus, for
 CC identifying agents having antiviral activity, and for treating viral
 CC disorders caused by retroviruses, rhadoviruses, or filoviruses. This
 CC sequence is a protein comprising the RING-SH complex of the invention.

SQ Sequence 497 AA;
Query Match 94.8%; Score 366; DB 7; Length 497;
Best Local Similarity 95.5%; Pred. No. 5e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARIVTGTTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDMKPSDPPWDQHAICY 60
Db 265 YEARIVTGTTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDMKPSDPPWDQHAICY 324
QY 61 PCKYL 66
Db 325 PCKYL 330

Search completed: March 10, 2004, 13:52:28
Job time : 51.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:52:35 ; Search time 29 Seconds
(without alignments)
480.556 Million cell updates/sec

Title: US-09-654-743-24

Perfect score: 386
Sequence: 1 YEARTVTGTWISYVKNKQL.....KPSDDPDQWQAKYPCGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 segs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	386	100.0	66	9	US-09-201-936-24
2	386	100.0	496	9	US-09-974-592-10
3	386	100.0	496	9	US-09-201-936-10
4	366	94.8	66	9	US-09-201-936-25
5	366	94.8	107	9	US-09-965-967-20
6	366	94.8	278	9	US-09-964-899-39
7	366	94.8	497	9	US-09-974-592-4
8	366	94.8	497	9	US-09-201-936-4
9	233	60.4	50	14	US-10-138-618-28
10	233	60.4	50	14	US-10-138-618-29
11	233	60.4	50	14	US-10-138-618-32
12	198	51.3	68	9	US-09-201-936-26
13	198	51.3	604	9	US-09-974-592-6
14	198	51.3	604	9	US-09-201-936-6
15	198	51.3	604	14	US-10-232-286-4

16	198	51.3	604	14	US-10-141-618-6	Sequence 6, Appli
17	198	51.3	1140	14	US-10-353-461-8	Sequence 8, Appli
18	190	49.2	68	9	US-09-201-936-28	Sequence 28, Appl
19	190	49.2	68	14	US-10-041-859-18	Sequence 18, Appl
20	190	49.2	172	14	US-10-041-859-12	Sequence 12, Appl
21	190	49.2	268	14	US-10-323-643-10	Sequence 10, Appl
22	189	49.0	600	9	US-09-974-592-12	Sequence 12, Appl
23	185	47.9	68	14	US-10-041-859-14	Sequence 14, Appl
24	185	47.9	172	14	US-10-041-859-8	Sequence 8, Appli
25	185	47.9	346	14	US-10-041-859-2	Sequence 2, Appli
26	184	47.7	68	9	US-09-201-936-27	Sequence 27, Appl
27	184	47.7	612	9	US-09-974-592-14	Sequence 14, Appl
28	184	47.7	612	14	US-10-232-286-14	Sequence 14, Appl
29	184	47.7	618	9	US-09-974-592-8	Sequence 8, Appli
30	184	47.7	618	9	US-09-201-936-8	Sequence 8, Appli
31	183	47.4	438	8	US-08-464-588-2	Sequence 2, Appli
32	183	47.4	438	14	US-10-323-643-2	Sequence 2, Appli
33	183	47.4	602	9	US-09-201-936-40	Sequence 40, Appl
34	183	47.4	618	14	US-10-153-668-338	Sequence 338, App
35	183	47.4	618	14	US-10-207-650-200	Sequence 200, App
36	183	47.4	618	14	US-10-232-286-2	Sequence 2, Appli
37	178	46.1	68	14	US-10-041-859-19	Sequence 19, Appl
38	178	46.1	109	9	US-09-965-967-30	Sequence 30, Appl
39	178	46.1	172	14	US-10-041-859-13	Sequence 13, Appl
40	178	46.1	591	9	US-09-201-936-42	Sequence 42, Appl
41	177	45.9	68	14	US-10-041-859-16	Sequence 16, Appl
42	177	45.9	172	14	US-10-041-859-10	Sequence 10, Appl
43	177	45.9	280	14	US-10-244-586-3	Sequence 3, Appli
44	177	45.9	298	14	US-10-235-026-2	Sequence 2, Appli
45	177	45.9	355	14	US-10-203-708-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-09-201-936-24
; Sequence 24, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneiluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT FILING DATE: 1998-12-01
; EARLIER FILING DATE: 1998-12-01
; EARLIER FILING DATE: 1998-02-04
; EARLIER FILING DATE: 1998-02-04
; EARLIER FILING DATE: 1996-08-05
; EARLIER FILING DATE: 1996-08-05
; EARLIER FILING DATE: 1995-12-22
; EARLIER FILING DATE: 1995-12-22
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-24

Query Match 100.0%; Score 386; DB 9; Length 66;
Best Local Similarity 100.0%; Pred. No. 4.4e-40;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARTVTGTWISYVKNKQLRAGFYALGEGDKVCKPCGGLTDWKPSDPWQHKAC 60

Db 1 YEARTVTGTWISYVKNKQLRAGFYALGEGDKVCKPCGGLTDWKPSDPWQHKAC 60

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QY 61 PGCKYL 66
Db 61 PGCKYL 66

US-09-974-592-10
RESULT 2
; Sequence 10, Application US/09974592
; Patent No. US2002012012A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-974-592-10

Query Match 100.0%; Score 386; DB 9; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.9e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPDQHAKCY 60
Db 264 YEARIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPDQHAKCY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

US-09-201-936-25
RESULT 4
; Sequence 25, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-25

Query Match 94.8%; Score 366; DB 9; Length 66;
Best Local Similarity 95.5%; Pred. No. 1.3e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPDQHAKCY 60
Db 1 YEARIVTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPDQHAKCY 60

QY 61 PGCKYL 66
Db 61 PGCKYL 66

US-09-965-967-20
RESULT 5
; Sequence 20, Application US/09965967
; Patent No. US2002017557A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yigong
; TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
; FILE REFERENCE: PU-0031 (01-1739-1)
; CURRENT APPLICATION NUMBER: US/09/965,967
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/236,574
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/256,830
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; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-967-20

Query Match          94.8%; Score 366; DB 9; Length 107;
Best Local Similarity 95.5%; Pred. No. 2.2e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTWTVSYNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPPDQHAKEY 60
Db 15 YEARIVTGTWTVSYNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPPDQHAKEY 74

QY 61 PGCKYL 66
Db 75 PGCKYL 80

RESULT 6
US-09-964-899-39
; Sequence 39, Application US/09964899
; Patent No. US2002017446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-964-899-39

Query Match          94.8%; Score 366; DB 9; Length 278;
Best Local Similarity 95.5%; Pred. No. 6.1e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTWTVSYNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPPDQHAKEY 60
Db 46 YEARIVTGTWTVSYNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPPDQHAKEY 105

QY 61 PGCKYL 66
Db 106 PGCKYL 111

RESULT 7
US-09-974-592-4
; Sequence 4, Application US/09974592
; Patent No. US2002012012A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
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; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-592-4

Query Match          94.8%; Score 366; DB 9; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.1e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTWTVSYNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPPDQHAKEY 60
Db 265 YEARIVTGTWTVSYNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPPDQHAKEY 324

QY 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 8
US-09-201-936-4
; Sequence 4, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-4

Query Match          94.8%; Score 366; DB 9; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.1e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTWTVSYNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPPDQHAKEY 60
Db 265 YEARIVTGTWTVSYNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPPDQHAKEY 324

QY 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 9
US-10-138-618-28
; Sequence 28, Application US/10138618
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Publication No. US20030100525A1
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-Nov-1997
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-138-618-28
Query Match 60.4%; Score 233; DB 14; Length 50;
Best Local Similarity 95.0%; Pred. No. 2,3e-21;
Matches 38; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 27 ALGEGDKVKCFHCGGLTDWKPSDDPDQWQAKYPCGCKYL 66
DB 1 ALGEGDKVKCFHCGGLTDWKPSDDPDQWQAKYPCGCKYL 40
RESULT 10
US-10-138-618-29
Sequence 29, Application US/10138618
Publication No. US20030100525A1
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-138-618-29
Query Match 60.4%; Score 233; DB 14; Length 50;
Best Local Similarity 95.0%; Pred. No. 2,3e-21;
Matches 38; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 27 ALGEGDKVKCFHCGGLTDWKPSDDPDQWQAKYPCGCKYL 66
DB 1 ALGEGDKVKCFHCGGLTDWKPSDDPDQWQAKYPCGCKYL 40
RESULT 11
US-10-138-618-32
Sequence 32, Application US/10138618
Publication No. US20030100525A1
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids


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; Sequence 4, Application US/10232286
; Publication No. US20030143579A1
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; Goedel, David V
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/232,286
; FILING DATE: 30-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,749
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 604 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-232-286-4

Query Match 51.3%; Score 198; DB 14; Length 604;
Best Local Similarity 55.9%; Pred. No. 7.le-16;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIIVTGTWYS--VNKEQLAPAGFYALGEGDKVKCFHCGGLTDWKPSDDPDQHAK 58
Db 255 HAAREKTFENWPSSVLVNPEQLASAGFYVGNDDVKFCDCGGLRCWESGDDPDWYQHAK 314
QY 59 CYPGCKYL 66
Db 315 WPPRCEYL 322

Search completed: March 10, 2004, 13:56:59
Job time : 29 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:49:29 ; Search time 13 Seconds
(without alignments)

488.357 Million cell updates/sec

Title: US-09-654-743-24

Perfect score: 386

Sequence: 1 YEARIIVFTGWIYSVNKEQL.....KPSEDPWDQAKYPCCKYL 66

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_78.*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	366	94.8	497	2 S69544	apoptosis inhibito
2	198	51.3	604	2 S68449	apoptosis inhibito
3	136	50.8	358	2 JCS964	apoptosis inhibito
4	130	49.2	268	2 T10304	inhibitor of apopt
5	130	49.2	268	2 A33989	apoptosis-inhibiti
6	184	47.7	618	2 S68450	apoptosis inhibito
7	177	45.9	298	2 JCT568	Kidney inhibitor o
8	175	45.3	275	2 A45679	inhibitor-of-apopt
9	164.5	42.6	1232	2 A5478	neuronal apoptosis
10	160.5	41.6	1447	2 T42628	apoptosis inhibito
11	149	38.6	496	2 S68452	apoptosis inhibito
12	149	38.6	497	2 S69545	apoptosis inhibito
13	141	36.5	208	2 T01183	probable apoptosis
14	128	33.2	275	2 T10310	apoptosis-inhibiti
15	126	32.6	150	2 T28409	ORF MSV248 probabl
16	114.5	29.7	4845	2 T31067	BR repeat contain
17	108	28.0	286	2 D36828	orf13 protein - Au
18	106	27.5	292	2 T41772	IAP1 orf27 - Bomby
19	100	25.9	155	2 T37471	apoptosis inhibito
20	99	25.6	155	2 T30489	apoptosis inhibito
21	93	24.1	308	2 T37474	apoptosis inhibito
22	84.5	21.9	997	2 T43523	cut17 protein - fi
23	83.5	21.6	329	2 T28403	ORF MSV242 probabl
24	80.5	20.9	564	2 C42523	A55R protein - vac
25	80.5	20.9	564	2 JQ1792	Salp17R protein -
26	66.5	17.2	187	2 T50621	hypothetical prote
27	66	17.1	511	2 T43634	nicotinic acetylch
28	66	17.1	534	2 T25720	hypothetical prote
29	65.5	17.0	737	2 PQ0219	RNA-2 polyprotein

30	65	16.8	466	2 PC4296	nicotinic acetylch
31	64.5	16.7	324	2 S39502	vegetative storage
32	64.5	16.7	506	2 S13720	coat protein - ara
33	64	16.3	204	2 H70609	probable dna-3-met
34	63	16.3	249	2 H72858	apoptosis inhibito
35	62.5	16.2	336	2 H81785	conserved hypotet
36	61.5	15.9	336	2 B81210	conserved hypotet
37	61.5	15.9	1808	2 T15099	hypothetical prote
38	60.5	15.7	437	2 AG0766	probable dehydrata
39	60.5	15.7	788	2 S70079	1,4-alpha-glucan b
40	60.5	15.7	1798	2 S53869	laminin beta-2 cha
41	60	15.5	246	2 I50127	MHC class II histo
42	60	15.5	249	2 T41814	IAP2 orf71 - Bomby
43	60	15.5	252	2 I50126	MHC class II histo
44	59.5	15.4	459	2 S76138	hypothetical prote
45	59.5	15.4	607	2 T39823	hypothetical prote

ALIGNMENTS

RESULT 1

S69544

apoptosis inhibitor IAP homolog - human

C.Species: Homo sapiens (man)

C.Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000

C.Accession: S69544; S68451

R.Duckett, C.S.; Nava, V.B.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, N

EMBO J. 15, 2685-2694, 1996

A.Title: A conserved family of cellular genes related to the baculovirus iap gene and

A.Reference number: S69544; MUID:96256286; PMID:8654366

A.Accession: S69544

A.Status: preliminary; nucleic acid sequence not shown

A.Molecule type: mRNA

A.Residues: 1-497 <DUC>

A.Cross-references: EMBL:U32974; NID:G1016687; PIDN:AAC50518.1; PID:G1016688

Riliston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Parahar

Nature 379, 349-353, 1996

A.Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of 1

A.Reference number: A58182; MUID:96149249; PMID:8552191

A.Accession: S68451

A.Status: nucleic acid sequence not shown

A.Molecule type: mRNA

A.Residues: 1-161, 'C', 163-422, 'Q', 424-497 <LIS>

A.Cross-references: EMBL:U45880; NID:G1184319; PIDN:AAC50373.1; PID:G1184320

A.Gene: ilp

C.Function:

A.Description: apoptotic suppressor

C.Superfamily: apoptosis inhibitor IAP homolog; RING finger homology

C.Keywords: apoptosis; zinc finger

F.446-490/Domain: RING finger homology <RRN>

Query Match 94.8%; Score 366; DB 2; Length 497;

Best Local Similarity 95.5%; Pred. No. 1.2e-33;

Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIIVFTGWIYSVNKEQLARAGFALGEGDKVKCFHCGGLTDWKPSEDPWDQAKCY 60

DB 265 YEARIIVFTGWIYSVNKEQLARAGFALGEGDKVKCFHCGGLTDWKPSEDPWDQAKWY 324

QY 61 PGCKYL 66

DB 325 PGCKYL 330

RESULT 2

S68449

apoptosis inhibitor hiap-1 - human

C.Species: Homo sapiens (man)

C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000

C.Accession: S68449

Riliston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Parahan

Nature 379, 349-353, 1996
A;Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A;Reference number: A58182; MUID:96149249; PMID:8552191

A;Accession: S68449
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-604 <LIS>
A;Cross-references: EMBL:U45878; NID:g1184315; PIDN:AAC50371.1; PID:g1184316
C;Function:
A;Description: apoptotic suppressor
C;Superfamily: RING finger homology
C;Keywords: apoptosis; zinc finger
F;553-597/Domain: RING finger homology <RNG>

Query Match 51.3%; Score 198; DB 2; Length 604;
Best Local Similarity 55.9%; Pred. No. 1.4e-14;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

Qy 1 YEARIIVFTGWIYS--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPDQHAH 58

Db 255 HAARFKTFNWPSSVLNPNQLASAGFYVGNSSDDVKCFCCDGLRCWESGDDPWVQHAH 314

Qy 59 CYPCKYL 66

Db 315 WFPRCYL 322

RESULT 3

JCS964
A;Title: Apoptosis inhibitor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 02-Sep-2000
C;Accession: JCS964
R;Stehlik, C.; de Martin, R.; Binder, B.R.; Lipp, J.
Biochem. Biophys. Res. Commun. 243, 827-832, 1998
A;Title: Cytokine induced expression of porcine inhibitor of apoptosis protein (IAP) fam
A;Reference number: JCS964; MUID:98162622; PMID:9501011
A;Accession: JCS964
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-358 <STE>
A;Cross-references: GB:U79142; NID:g2957174; PIDN:AAC39171.1; PID:g2957175
C;Superfamily: RING finger homology
F;307-351/Domain: RING finger homology <RRN>

Query Match 50.8%; Score 196; DB 2; Length 358;
Best Local Similarity 54.4%; Pred. No. 1.4e-14;
Matches 37; Conservative 7; Mismatches 22; Indels 2; Gaps 1;

Qy 1 YEARIIVFTGWIYS--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPDQHAH 58

Db 90 YAAARFKTFNWPSSIPVHPQLASAGFYVGNSSDDVKCFCCDGLRCWESGDDPWVQHAH 149

Qy 59 CYPCKYL 66

Db 150 WFPRCYL 157

RESULT 4

T10304
A;Title: Inhibitor of apoptosis protein 3 - Orgyia pseudotsugata nuclear polyhedrosis virus
C;Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpNPV
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000
C;Accession: T10304
R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virology 229, 381-399, 1997
A;Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis
A;Reference number: Z17011; MUID:97271300; PMID:9126251
A;Accession: T10304
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-268 <AHR>
A;Cross-references: EMBL:U75930; NID:g2934903; PIDN:AAC59034.1; PID:g1911281

C;Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F;217-261/Domain: RING finger homology <RNG>

Query Match 49.2%; Score 190; DB 2; Length 268;

Best Local Similarity 48.5%; Pred. No. 5.2e-14;

Matches 32; Conservative 12; Mismatches 20; Indels 2; Gaps 1;

Qy 3 ARIVTFGTWIVSNK--EQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPDQHAH 60

Db 113 ARLRTFAEWPRLKQRPBELAEGFFYTGQDKTRCFCCDGLKDWEPDDAPWQHAHWY 172

Qy 61 PGCKYL 66

Db 173 DRCEYV 178

RESULT 5

A53989
A;Title: Apoptosis-inhibiting protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis
C;Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpNPV
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 15-Sep-2000
C;Accession: A53989
R;Birbaum, M.J.; Clem, R.J.; Miller, L.K.
J. Virol. 68, 2521-2528, 1994
A;Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a po
A;Reference number: A53989; MUID:94187094; PMID:8139034
A;Accession: A53989
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-268 <BIR>
A;Cross-references: GB:L22564; NID:g456111; PIDN:AAB02610.1; PID:g456114
A;Note: authors translated the codon TGG for residue 28 as TTT, GAC for residue 50 as
C;Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F;217-261/Domain: RING finger homology <RRN>

Query Match 49.2%; Score 190; DB 2; Length 268;

Best Local Similarity 48.5%; Pred. No. 5.2e-14;

Matches 32; Conservative 12; Mismatches 20; Indels 2; Gaps 1;

Qy 3 ARIVTFGTWIVSNK--EQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPDQHAH 60

Db 113 ARLRTFAEWPRLKQRPBELAEGFFYTGQDKTRCFCCDGLKDWEPDDAPWQHAHWY 172

Qy 61 PGCKYL 66

Db 173 DRCEYV 178

A:Residues: 1-36, 'A', 37, 'K', 38, 'L', 41-44, 'H', 46-58, 'Q', 60-612, 'A', 643-647, 'A', 649-6498
A:Cross-references: EMBL:U45881; NID:g1184313; PIDN:AAC46988.1; PID:g1184314
C:Genetics:
A:Cross-references: FlyBase:Fgn0015247
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C:Keywords: apoptosis; zinc finger
F:445-449/Domain: RING finger homology <RNG>

RESULT 14
T01310
apoptosis-inhibiting protein 1 - Orgyia pseudotsugata nuclear polyhedrosis virus
C:Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OPMNPV
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000
C:Accession: T01310
R:Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virology 229, 381-399, 1997
A:Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus
A:Reference number: Z17011; MUID:97271300; PMID:9126351

C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69545
R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M.C.
EMBO J. 15, 2685-2694, 1996
A:Title: A conserved family of cellular genes related to the baculovirus iap gene and encoding a novel protein
A:Reference number: S69544; MUID:96256286; PMID:8654366
A:Accession: S69545
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DUC>
A:Cross-references: EMBL:U32373; NID:g1019116; PIDN:AAC47155.1; PID:g1019117
C:Genetics:
A:Gene: ilp
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C:445-490/Domain: RING finger homology <RRN>

ORF MS248 probable inhibitor of apoptosis protein (IAP) - *Melanoplus sanguinipes*
C.Species: *Melanoplus sanguinipes* entomopoxvirus
C.Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C.Accession: T28409
R.Afonso, C.L.; Tullman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A.Title: The genome of *Melanoplus sanguinipes* entomopoxvirus.
A.Reference number: Z20484; MUID:99102612; PMID:9847359
A.Accession: T28409
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA

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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:42:54 ; Search time 10.5 Seconds

(without alignments)
327.298 Million cell updates/sec

Title: US-09-654-743-24

Perfect score: 386

Sequence: 1 YEARIVTGTWYSVNEQL.....KPSDFWDQAKYPCCKYL 66

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	366	94.8	BIR4 RAT	Q9016 rattus norv
2	366	94.8	BIR4 HUMAN	P38170 homo sapien
3	357	92.5	BIR4 MOUSE	Q06989 mus musculu
4	334	86.5	BIR8 HUMAN	Q96p09 homo sapien
5	328	85.0	BIR8 PANTR	Q95m72 pan troglod
6	325	84.2	BIR8 GORGO	Q95m71 gorilla gor
7	198	51.3	BIR3 HUMAN	Q13489 homo sapien
8	186	50.8	BIRP BIG	Q62640 sus scrofa
9	182	49.7	BIR CHICK	Q90680 gallus gall
10	190	49.2	IAP3 NPVOP	P41437 orgyia pseu
11	189	49.0	BIR3 MOUSE	Q08863 mus musculu
12	184	47.7	BIR2 MOUSE	Q62210 mus musculu
13	183	47.4	BIR2 HUMAN	Q13490 homo sapien
14	178	46.1	IAP1 DROME	Q24306 drosophila
15	177	45.9	BIR7 HUMAN	Q96ca5 homo sapien
16	175	45.3	IAP GUPC	P41436 cydia pomon
17	164.5	42.6	BIR1 HUMAN	Q13075 homo sapien
18	164.5	42.6	BIRP MOUSE	Q9j1b6 mus musculu
19	163.5	42.4	BIRG MOUSE	Q9j1b3 mus musculu
20	163.5	42.4	BIRG MOUSE	Q9gwk5 mus musculu
21	163.5	42.4	BIRB MOUSE	Q9r016 mus musculu
22	160.5	41.6	IAPB DROME	Q9gk4 mus musculu
23	149	38.6	IAP2 DROME	Q24307 drosophila
24	141	36.5	ZFP IRV6	P47732 chilo iride
25	128	33.2	IAP1 NPVOP	O10296 orgyia pseu
26	121.5	31.5	BIR5 RAT	Q9jhy7 rattus norv
27	119.5	31.0	BIR5 MOUSE	O70201 mus musculu
28	114.5	29.7	BIR5 HUMAN	O15392 homo sapien
29	114.5	29.7	BIR6 HUMAN	Q9nr09 homo sapien
30	108	28.0	IAP1 NPVAC	P41435 autographa
31	84.5	21.9	BIR1 SCHPO	O4064 schizosacch
32	80.5	20.9	VA55_VACCC	P21073 vaccinia vi
33	80.5	20.9	VA55_VACCV	P24768 vaccinia vi

ALIGNMENTS

```

RESULT 1
BIR4 RAT
ID BIR4 RAT STANDARD; PRT; 436 AA.
AC Q9R016;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (RIAP3) (RIAP-3).
GN BIRC4 OR API3 OR XIAP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Sato N.;
RT "Rattus norvegicus X-linked inhibitor of apoptosis (riap3) mRNA.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
CC (By similarity).
CC -!- SUBUNIT: Interacts with SMAC and with PRS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRS25 are mediated by the second
CC and third BIR domains (By similarity).
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
-----
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or send an email to license@isb-sib.ch).
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EMBL; AB033366; BAA85304.1; -
HSSP; Q13490; 10EH.
InterPro; IPR001370; BIR.
Pfam; PF00653; BIR; 3
SMART; SM00238; BIR; 3.
SMART; SM00184; RING; 1.
PROSITE; PS01282; BIR_REPEAT_1; 3.
PROSITE; PS0143; BIR_REPEAT_2; 3.
PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
PROSITE; PS00518; ZF_RING_2; 1.
AP00518; ZF_RING_2; 1.
AP00518; Zinc-finger; Repeat.
REPEAT 26 93
REPEAT 163 230
REPEAT 264 329
BIR 1.
BIR 2.
BIR 3.

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DR PROSITE; PS00143; BIR_REPEAT 2; 3.
DR PROSITE; PS00518; ZF_RING 1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING 2; 1.
KW Apoptosis; Zinc-finger; Repeat; Thiol protease inhibitor;
KW 3D-structure.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 265 330 BIR 3.
FT ZN_FING 450 485 RING-TYPE.
FT MUTAGEN 214 214 D->S; REDUCED INTERACTION WITH PRSS25.
FT MUTAGEN 314 314 E->S; DECREASED INTERACTION WITH SMAC AND WITH PRSS25.
FT CONFLICT 162 162 S -> C (IN REF. 1).
FT CONFLICT 423 423 Q -> P (IN REF. 2).
SQ SEQUENCE 497 AA; 56684 MW; 9D394C16D45EB635 CRC64;

Query Match 94.8%; Score 366; DB 1; Length 497;
Best Local Similarity 95.5%; Pred.No. 3.4e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIIVFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQAKCY 60
DB 265 YEARIIVFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQAKCY 324
QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 3
BIR4_MOUSE STANDARD; PRT; 496 AA.
AC Q60859; O08865;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (MIAP3) (MIAP-3).
GN BIRC4 OR A213 OR XIAP OR AIPA OR MIHA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978 (1996).
RN [2]
RN SEQUENCE FROM N.A.
RA Farahani R., Lefebvre C., Korneluk R.G., Mackenzie A.E.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
CC (By similarity).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRSS25 are mediated by the second
CC and third BIR domains (By similarity).
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC -----
DR EMBL; U36842; AAC52594.1; -.
DR EMBL; U88990; AAB58376.1; -.
DR HSSP; Q13490; 1QBH.
DR MGD; MGI:107572; Birc4.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF06553; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT 1; 3.
DR PROSITE; PS0143; BIR_REPEAT 2; 3.
DR PROSITE; PS00518; ZF_RING 1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING 2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 264 329 BIR 3.
FT ZN_FING 449 484 RING-TYPE.
FT CONFLICT 208 208 E -> K (IN REF. 2).
FT CONFLICT 317 317 E -> D (IN REF. 2).
FT CONFLICT 322 322 W -> C (IN REF. 2).
FT CONFLICT 346 346 S -> P (IN REF. 2).
FT CONFLICT 360 360 S -> P (IN REF. 2).
FT CONFLICT 388 388 I -> L (IN REF. 2).
FT CONFLICT 449 449 C -> S (IN REF. 2).
FT CONFLICT 462 462 V -> F (IN REF. 2).
FT CONFLICT 468 468 V -> A (IN REF. 2).
FT CONFLICT 490 490 K -> N (IN REF. 2).
SQ SEQUENCE 496 AA; 56079 MW; ECSFAE0799F2CDD8 CRC64;

Query Match 92.5%; Score 357; DB 1; Length 496;
Best Local Similarity 93.9%; Pred.No. 4e-35;
Matches 62; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YEARIIVFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQAKCY 60
DB 264 YEARIIVFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQAKCY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 4
BIR8_HUMAN STANDARD; PRT; 236 AA.
AC Q96P09; Q96RW5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2) (Testis-specific
DE inhibitor of apoptosis).
GN BIRC8 OR ILP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=21481900; PubMed=11597143;
RA Lagace M., Xuan J.-Y., Young S.S., McRoberts C., Maier J.,
RA Rajcan-Separovic E., Korneluk R.G.;
RT "Genomic organization of the X-linked inhibitor of apoptosis and
RT identification of a novel testis-specific transcript."
RL Genomics 77:181-188 (2001).
RN [2]

```

Frattini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
Notarangelo L.D., Vezzoni P., Fearhead H.O., Duckett C.S.;
"Molecular cloning of ILP-2, a novel member of the inhibitor of
apoptosis protein family";
Mol. Cell. Biol. 21:4292-4301(2001).
-1- FUNCTION: Protects against apoptosis mediated by BAX (By
similarity).
-1- SUBUNIT: Binds to caspase-9 (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-1- SIMILARITY: Belongs to the IAP family.
-1- SIMILARITY: Contains 1 BIR repeat.
-1- SIMILARITY: Contains 1 RING-type zinc finger.

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EMBL; AY030052; AK49776.1; --
InterPro; IPR001370; BIR.
InterPro; IPR001841; Znf_ring.
Pfam; PF00653; BIR; 1.
SMART; SM00238; BIR; 1.
SMART; SM00184; RING; 1.
PROSITE; PS01282; BIR_REPEAT_1; 1.
PROSITE; PS0143; BIR_REPEAT_2; 1.
PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
PROSITE; PS00089; ZF_RING_2; 1.
Apoptosis; Zinc-finger.
REPEAT 7 70
ZN_FING 189 224 RING-TYPE.
SEQUENCE 236 AA; 27136 MW; 64CCA3A251420EDE CRC64;

Query March 85.0%; Score 328; DB 1; Length 236;
Best Local Similarity 80.3%; Pred. NO. 5.5e-32;
Matches 53; Conservative 8; Mismatches 5; Indels 0; Gaps 0

QY 1 YEARIIVFTGWTIVSYNKEQLARAGFYALGEGDKVKCFHCGGLTWKSGEDPDWQHAKY 60
4 YEASLIITFTGWTIVSYNKEQLARAGFYALGEGDKVKCFHCGGLTWKSGEDPDWQHAKY 63

QY 61 PGCKYL 66
DB 64 PGCKYL 69

RESULT 6
BIR8 GORGO
ID BIR8 GORGO STANDARD; PRT; 236 AA.
AC Q9SM71;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (inhibitor of apoptosis-
like protein 2) (IAP-like protein 2) (ILP-2).
GN BIRCS OR ILP2
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
NCBI_TaxID=9595;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=21286921; PubMed=11390657;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Reffey S.B.,
RA Frattini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezzoni P., Fearhead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
apoptosis protein family";
RT Mol. Cell. Biol. 21:4292-4301(2001).
CC -1- FUNCTION: Protects against apoptosis mediated by BAX (By

```
CC similarity).
CC -!- SUBUNIT: Binds to caspase-9 (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 1 BIR repeat.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC -----
CC EMBL; AY030053; AK49777.1; -.
CC InterPro; IPR001370; BIR.
CC InterPro; IPR001841; Znf_ring.
CC Pfam; PF00653; BIR; 1.
CC SMART; SM00238; BIR; 1.
CC SMART; SM00184; RING; 1.
CC PROSITE; PS01282; BIR_REPEAT_1; FALSE_NEG.
CC PROSITE; PS0143; BIR_REPEAT_2; 1.
CC PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
CC PROSITE; PS00089; ZF_RING_2; 1.
CC KW Apoptosis; Zinc-finger.
CC FT REPEAT 7 70 RING.
CC FT ZN FING 189 224 RING-TYPE.
CC SEQUENCE 236 AA; 27120 MW; C3A70B39BE442E4C CRC64;
CC -----
Query Match 84.2%; Score 325; DB 1; Length 236;
Best Local Similarity 78.8%; Pred. NO. 1.3e-31;
Matches 52; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
CC
CC QY 1 YEAVITFTWTIYSVYNKQLRAGFYALGEGDKVKCFHCGGGLTDWKPSPDPWDQAKCY 60
CC DB |||||
CC 4 YEAVITFTWTIYSVYNKQLRAGFYALGEGDKVKCFHCGGGLANWPKEDPWEQAKWY 63
CC
CC QY 61 PGCKYL 66
CC DB |||||
CC 64 PGCKYL 69
CC
CC RESULT 7
CC BIR3_HUMAN STANDARD; PRT; 604 AA.
CC ID BIR3_HUMAN Q13489; Q16628; Q9HC27; Q9UP46;
CC AC Q13489; Q16628; Q9HC27; Q9UP46;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis
CC DE protein 1) (HIAP1) (HIAP-1) (C-IAP2) (TNFR2-TRAF signaling complex
CC DE protein 1) (IAP homolog C) (Apoptosis inhibitor 2) (API2).
CC GN BIRC3 OR API2 OR IAP1 OR MIHC.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxId=9606;
CC [1]
CC RN SEQUENCE FROM N.A.
CC RX MEDLINE=96128127; PubMed=8548810;
CC Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
CC RT "The TNFR2-TRAF signaling complex contains two novel proteins related
CC RT to baculoviral inhibitor of apoptosis proteins.";
CC RL Cell 83:1243-1252 (1995).
CC [2]
CC RN SEQUENCE FROM N.A.
CC RC TISSUE=Liver;
CC RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
CC Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
CC RT "Suppression of apoptosis in mammalian cells by NAIP and a related
CC RT family of IAP genes.";
```

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RL Nature 379:349-353 (1996).
RN [3]
RN SEQUENCE FROM N.A.
RP TISSUE=Fetal liver;
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT receptor-associated factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978 (1996).
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE=99252096; PubMed=10233894;
RA Horrevorts A.J., Fontijn R.D., van Zonneveld A.J., de Vries C.J.,
RA ten Cate J.W., Pannekoek H.;
RT "Vascular endothelial genes that are responsive to tumor necrosis
RT factor-alpha in vitro are expressed in atherosclerotic lesions,
RT including inhibitor of apoptosis protein-1, stannin, and two novel
RT genes.";
RN Blood 93:3418-3431 (1999).
RN [5]
RN SEQUENCE FROM N.A.
RP TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RN SEQUENCE OF 362-441 FROM N.A.
RX MEDLINE=20519161; PubMed=11066071;
RA Baens M., Steyls A., Dierlam J., De Wolf-Peeters C., Marynen P.;
RT "Structure of the M1 gene and molecular characterization of the
RT genomic breakpoint junctions in the t(11;18)(q21;q21) of marginal zone
RT B-cell lymphomas of MALT type.";
RL Genes Chromosomes Cancer 29:281-291 (2000).
CC -!- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL LUNG, AND KIDNEY. IN
CC THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES,
CC INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.
CC -!- DISEASE: Involved in a t(11;18)(q21;q21) chromosomal translocation
CC recurrent in low-grade MALT lymphoma (Mucosa-associated lymphoid
CC tissue). This translocation is found in approximately 50% of
CC cytogenetically abnormal low-grade MALT lymphoma and involves
CC MALT1 and BIRC3.
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -!- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobogen.fr/services/chromocancer/BIRC3ID239.html".
```

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EMBL; L49432; AAC41943.1; -
EMBL; U45878; AAC50371.1; -
EMBL; U37546; AAC50507.1; -
EMBL; AF070674; AAC83232.1; -
EMBL; BC037420; AAH37420.1; -
EMBL; AF178945; AAC09369.1; -
PIR; S68449; S68449.
HSP; Q13490; IQBH.
Genew; HGNC:591; BIRC3.
MIM; 601721.
GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
GO; GO:0006916; P:anti-apoptosis; TAS.
GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
InterPro; IPR001370; BIR.
InterPro; IPR001315; CARD.
InterPro; IPR001841; Znf_ring.
Pfam; PF00653; BIR; 3.
Pfam; PF00619; CARD; 1.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00238; BIR; 3.
SMART; SM00114; CARD; 1.
SMART; SM00184; RING; 1.
PROSITE; PS01282; BIR_REPEAT_1; 3.
PROSITE; PS0143; BIR_REPEAT_2; 3.
PROSITE; PS50209; CARD; 1.
PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
PROSITE; PS50089; ZF_RING_2; 1.
Apoptosis; Zinc-finger; Repeat; Chromosomal translocation.
REPEAT 29 96
REPEAT 169 235
REPEAT 255 322
REPEAT 439 529
DOMAIN 557 592
ZN_FING 557 592
SITE 442 443
BIR_C3-WALT1.
N -> Y (IN REF. 4).
N -> H (IN REF. 2).
D -> E (IN REF. 2).
H -> P (IN REF. 2).
A -> P (IN REF. 2).
K -> R (IN REF. 2).
F -> L (IN REF. 2).
Q -> P (IN REF. 2).
SEQUENCE 604 AA; 68371 MW; 8581AC0BA9AAB4A7 CRC64;
Query Match 51.3%; Score 198; DB 1; Length 604;
Best Local Similarity 55.9%; Pred. No. 5e-16;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;
QY 1 YEARIIVTGTWYS--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPESDPWDQHAH 58
DB 255 HAARFKTFENPSSVLNPEQLASAGFYVYVNSDDVKCFCCDGLRCWESGDDPWVQHAH 314
QY 59 CYPGCKYL 66
DB 315 WFPRCYEL 322
RESULT 8
PIAP PIG STANDARD; PRT; 358 AA.
AC O62840;
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE Inhibitor of apoptosis protein (IAP) (Inhibitor of T cell apoptosis)
```

```
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative inhibitor of apoptosis.
GN PIAP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RA MEDLINE=98162622; PubMed=9501011;
RX Stehlik C., de Martin R., Binder B.R., Lipp J.;
RT "Cytokine induced expression of porcine inhibitor of apoptosis
protein (Iap) family member is regulated by NF-kappa B.";
RL Biochem. Biophys. Res. Commun. 243:827-832(1998).
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 2 BIR repeats.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
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EMBL; U79142; AAC39171.1; -
PIR; JCS964; JCS964.
HSP; Q13490; IQBH.
InterPro; IPR001370; BIR.
InterPro; IPR001315; CARD.
InterPro; IPR001841; Znf_ring.
Pfam; PF00653; BIR; 2.
Pfam; PF00619; CARD; 1.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00238; BIR; 2.
SMART; SM00114; CARD; 1.
SMART; SM00184; RING; 1.
PROSITE; PS01282; BIR_REPEAT_1; 2.
PROSITE; PS0143; BIR_REPEAT_2; 2.
PROSITE; PS50209; CARD; 1.
PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
PROSITE; PS50089; ZF_RING_2; 1.
Apoptosis; Zinc-finger; Repeat.
REPEAT 4 70
REPEAT 90 157
REPEAT 193 283
DOMAIN 311 346
ZN_FING 311 346
RING-TYPE.
SEQUENCE 358 AA; 40977 MW; EB2268FA9A6190A4 CRC64;
Query Match 50.8%; Score 196; DB 1; Length 358;
Best Local Similarity 54.4%; Pred. No. 5e-16;
Matches 37; Conservative 7; Mismatches 22; Indels 2; Gaps 1;
QY 1 YEARIIVTGTWYS--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPESDPWDQHAH 58
DB 90 YAARFKTFENPSSVLPVHPEQLASAGFYVYVNSDDVKCFCCDGLRCWESGDDPWVQHAH 149
QY 59 CYPGCKYL 66
DB 150 WFPRCYEL 157
RESULT 9
BIR_CHICK
ID BIR_CHICK STANDARD; PRT; 611 AA.
AC Q90660; O57319;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Inhibitor of apoptosis protein (IAP) (Inhibitor of T cell apoptosis)
```

DE protein).

GN ITPA OR IAP1.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archozoa; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OC NCBI_TaxID=9031;

RN [1] _TaxID=9031;

RP SEQUENCE FROM N.A.

RC TISSUE=Splicein;

RX MEDLINE=97101112; PubMed=8945639;

RA Digby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal J.W.;

RT "ITA, a vertebrate homologue of IAP that is expressed in T

RL lymphocytes.";

RL DNA Cell Biol. 15:981-988(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=White leghorn; TISSUE=Embryonic fibroblast;

RX MEDLINE=98038801; PubMed=9372964;

RA You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;

RT "ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a

RL mediator of the antiapoptotic activity of the v-Rel oncoprotein.";

RL Mol. Cell. Biol. 17:7328-7341(1997).

CC -!- FUNCTION: Apoptotic suppressor.

CC -!- SUBCELLULAR LOCATION: Predominantly nuclear. Cytoplasmic

CC according to Ref.2.

CC -!- TISSUE SPECIFICITY: Cells of the T lymphocyte lineage. Found in

CC both cortical and medullary cells of the thymus. Expressed at

CC relatively high levels also in spleen, bursa, intestine and lung

CC and at very low levels in testis, brain and skeletal muscle.

CC -!- INDUCTION: High levels are induced within 4-8 hours of T-cell

CC activation in spleen and thymus.

CC -!- DOMAIN: The ring finger is important for its antiapoptotic effect.

CC -!- SIMILARITY: Belongs to the IAP family.

CC -!- SIMILARITY: Contains 3 BIR repeats.

CC -!- SIMILARITY: Contains 1 CARD domain.

CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; U27466; AAB48118.1; -.

DR EMBL; AF008592; AAB88044.1; -.

DR HSSP; Q13490; 1QBH.

DR InterPro; IPR001370; BIR.

DR InterPro; IPR001315; CARD.

DR InterPro; IPR001841; Znf_ring.

DR Pfam; PF00853; BIR; 3.

DR Pfam; PF00619; CARD; 1.

DR Pfam; PF00097; ZF-C3HC4; 1.

DR SMART; SM00238; BIR; 3.

DR SMART; SM00114; CARD; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01282; BIR_REPEAT_1; 3.

DR PROSITE; PS01433; BIR_REPEAT_2; 3.

DR PROSITE; PS00209; CARD; 1.

DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.

DR PROSITE; PS00089; ZF_RING_2; 1.

DR Apoptosis; Zinc-finger; Repeat; Nuclear protein.

FT REPEAT 30 97 BIR 1.

FT REPEAT 176 242 BIR 2.

FT REPEAT 262 329 BIR 3.

FT DOMAIN 446 536 CARD.

FT ZN FING 564 599 RING-TYPE.

FT CONFLICT 27 27 F -> L (IN REF. 2).

FT CONFLICT 150 150 R -> Q (IN REF. 2).

FT CONFLICT 169 169 Q -> H (IN REF. 2).

FT CONFLICT 193 193 S -> F (IN REF. 2).

FT CONFLICT 190 192 CLW -> FLS (IN REF. 2).

FT CONFLICT 196 196 V -> L (IN REF. 2).

FT CONFLICT 202 203 DD -> YY (IN REF. 2).

FT CONFLICT 213 214 VN -> FT (IN REF. 2).

FT CONFLICT 217 218 VK -> GQ (IN REF. 2).

FT CONFLICT 350 355 WNSST -> EQLS (IN REF. 2).

FT CONFLICT 359 359 K -> T (IN REF. 2).

FT CONFLICT 426 426 E -> D (IN REF. 2).

FT CONFLICT 492 492 T -> K (IN REF. 2).

FT CONFLICT 497 497 S -> L (IN REF. 2).

FT CONFLICT 524 524 F -> C (IN REF. 2).

SQ SEQUENCE 611 AA; 69009 MW; 53FC9136F34EBDD CRC64;

Query Match 49.7%; Score 192; DB 1; Length 611;

Best Local Similarity 52.9%; Pred. No. 2.6e-15;

Matches 36; Conservative 8; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIIVFTGW--IYSVVKQLARAGYALGEGBKVKCFHCGGLTDWKPSEDPWQHAH 58

Db 262 HEARVKTFINWPTIPVQPEQLADAGFYVYVRNDVKFCDCDGLRCWESGDDPWIEHAK 321

QY 59 CYPGCKYL 66

Db 322 WFPRCYL 329

RESULT 10

IAP3_NPVOP

ID IAP3_NPVOP STANDARD; PRT; 268 AA.

AC P41437;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Apoptosis inhibitor 3 (IAP-3).

GN IAP3 OR IAP.

OS Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).

OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;

OC Nucleopolyhedrovirus.

OX NCBI_TaxID=164623;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94187094; PubMed=8139034;

RA Birnbaum M.J., Clem R.J., Miller L.K.;

RT "An apoptosis-inhibiting gene from a nuclear polyhedrosis virus

RT encoding a polypeptide with Cys/His sequence motifs.";

RL J. Virol. 68:2521-2528(1994).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=97271300; PubMed=9126251;

RA Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,

RA Rohmann G.F.;

RT "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear

RT polyhedrosis virus genome.";

RL Virology 229:381-395(1997).

CC -!- FUNCTION: ACTS BY BLOCKING CELLULAR APOPTOSIS RATHER THAN BY

CC PREVENTING VIRAL STIMULATION OF APOPTOSIS.

CC -!- SIMILARITY: Contains 2 BIR repeats.

CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

CC -----

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CC -----

DR EMBL; L22564; AAB02610.1; -.

DR EMBL; U75930; AAC59034.1; -.

DR PIR; A53989; A53989.

DR HSSP; Q13490; 1QBH.

DR InterPro; IPR001370; BIR.

DR InterPro; IPR001841; Znf_ring.

```

DR Pfam; PF00653; BIR; 2.
DR SMART; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 2.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 2.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR PROSITE; ZINC-finger; Repeat.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 18 84 BIR 1.
FT REPEAT 111 178 BIR 2.
FT ZN FING 221 256 RING-TYPE.
SQ SEQUENCE 268 AA; 30076 MW; DF89175FDB85A708 CRC64;

Query Match 49.2%; Score 190; DB 1; Length 268;
Best Local Similarity 48.5%; Pred. No. 2e-15;
Matches 32; Conservative 12; Mismatches 20; Indels 2; Gaps 1;

QY 3 ARIVTFGTWISYK--EOLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWQHAQY 60
DB 113 ARIRTAENPRGLKQRPPELLAEGFFYTGQKTRCFCCDGLKDWEPDDAPWQHAQY 172

QY 61 PGCKYL 66
DB 173 DRCEYV 178

RESULT 11
BIR3_MOUSE STANDARD; PRT; 600 AA.
AC O08863;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis
protein 1) (MIAP1) (MIAP-1).
GN BIRC3 OR BIRC2 OR IAP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
EN 1 and 2 genes."
RN SEQUENCE FROM N.A.
RP TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
1 and 2 genes."
RL Genomics 46:495-503(1997).
CC -!- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY).
CC -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U88908; AAC53531.1; --
DR HSPB; Q13490; IQBH.
DR MGB; MGI:1197007; Birc2.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS02029; CARD; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR PROSITE; ZINC-finger; Repeat.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 127 94 BIR 1.
FT REPEAT 167 233 BIR 2.
FT REPEAT 253 320 BIR 3.
FT DOMAIN 436 525 CARD.
FT ZN FING 553 588 RING-TYPE.
SQ SEQUENCE 600 AA; 67198 MW; AD7F73E6849317D1 CRC64;

Query Match 49.0%; Score 189; DB 1; Length 600;
Best Local Similarity 51.5%; Pred. No. 5.9e-15;
Matches 35; Conservative 9; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIVTFGTWISY--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWQHAQ 58
DB 253 HAARITFTSNPSSALVHSQELASAGFYTYTGHSDVKFCDCDGLRCWESGDDPWVEHAK 312

QY 59 CYPGCKYL 66
DB 313 WPFRCYEL 320

RESULT 12
BIR2_MOUSE STANDARD; PRT; 612 AA.
AC Q62210; O08864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis
protein 2) (MIAP2) (MIAP-2).
GN BIRC2 OR BIRC3 OR IAP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
EN 1 and 2 genes."
RN SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RP TISSUE=Skeletal muscle;
RX MEDLINE=96128127; PubMed=8548810;
RA Rothe M., Fan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins."
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RP TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
1 and 2 genes."
RL Genomics 46:495-503(1997).
CC -!- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in heart, brain, spleen, lung,
CC liver, skeletal muscle, kidney and testis.
CC -!- SIMILARITY: Belongs to the IAP family.

```


CC -!- SIMILARITY: Contains 3 BIR repeats.
 CC -!- SIMILARITY: Contains 1 CARD domain.
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -----
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 CC -----
 CC EMBL: L49433; AAC42078.1; -
 CC EMBL: U88909; AAC53532.1; -
 CC HSSP: Q13490; IQBH.
 CC MGD: MG1:1197009; Birc3.
 CC InterPro: IPR001370; BIR.
 CC InterPro: IPR001315; CARD.
 CC InterPro: IPR001841; Znf_ring.
 CC Pfam: PF00653; BIR; 3.
 CC Pfam: PF00619; CARD; 1.
 CC Pfam: PF00097; Zf-C3HC4; 1.
 CC SMART: SM00238; BIR; 3.
 CC SMART: SM00114; CARD; 1.
 CC SMART: SM00184; RING; 1.
 CC PROSITE: PS01282; BIR_REPEAT_1; 3.
 CC PROSITE: PS0143; BIR_REPEAT_2; 3.
 CC PROSITE: PS0209; CARD; 1.
 CC PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 CC PROSITE: PS00509; ZF_RING_2; 1.
 CC Apoptosis; Zinc-finger; Repeat.
 KW REPEAT 46 113
 FT REPEAT 177 243
 FT REPEAT 262 329
 FT DOMAIN 447 537
 FT ZN FING 565 600
 FT CONFLICT 380 380
 FT SEQUENCE 612 AA; 69676 MW; E0896D93C6C610D CRC64;
 SQ
 Query Match 47.7%; Score 184; DB 1; Length 612;
 Best Local Similarity 51.5%; Pred. No. 2.4e-14;
 Matches 35; Conservative 9; Mismatches 22; Indels 2; Gaps 1;
 QY 1 YEARTVITGTWYS--VNKEQLARAGFYALGEGDKVCFHCGGGLTDWKPSDPPDQHAH 58
 Db 262 HSARLRTFLYPPSPVQPEQLASGFFYVDRNDVKFCDCGGLRCWEGDDPWIEHAK 321
 QY 59 CYPGCKYL 66
 Db 322 WPPRCFEL 329
 RESULT 13
 BIR2_HUMAN
 ID BIR2_HUMAN STANDARD; PRT; 618 AA.
 AC Q13490; Q16516;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 2 (inhibitor of apoptosis
 DE protein 2) (HAP2) (HAP-2) (C-IAP1) (TNFR2-TRAF signaling complex
 DE protein 2) (IAP homolog B).
 GN BIR2 OR AP1 OR IAP2 OR MIB1.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=96128127; PubMed=8548810;
 RX Rother M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
 RA "The TNFR2-TRAF signaling complex contains two novel proteins related
 RT to baculoviral inhibitor of apoptosis proteins.";

RL Cell 83:1243-1252(1995).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96149249; PubMed=8552191;
 RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
 RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
 RT "Suppression of apoptosis in mammalian cells by NAIP and a related
 RT family of IAP genes.";
 RL Nature 379:349-353(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=96209843; PubMed=8643514;
 RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
 RT "Cloning and expression of apoptosis inhibitory protein homologs that
 RT function to inhibit apoptosis and/or bind tumor necrosis factor
 RT receptor-associated factors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis, and Uterus;
 RX MEDLINE=23388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP STRUCTURE BY NMR OF 266-363.
 RX MEDLINE=9932054; PubMed=10404221;
 RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;
 RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP)
 RT repeat.";
 RL Nat. Struct. Biol. 6:648-651(1999).
 CC -!- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
 CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
 CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
 CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
 CC -!- SUBUNIT: Interacts with SMAC and with PRS25; these interactions
 CC inhibit apoptotic suppressor activity.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (potential).
 CC -!- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.
 CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,
 CC AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD
 CC LEUKOCYTES.
 CC -!- SIMILARITY: Belongs to the IAP family.
 CC -!- SIMILARITY: Contains 3 BIR repeats.
 CC -!- SIMILARITY: Contains 1 CARD domain.
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
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 CC -----


```
CC EMBL; L49431; AAC41942.1; -
DR GO; GO:0008189; P:apoptosis inhibitor activity; TAS.
DR EMBL; U45879; AAC50372.1; -
DR EMBL; U37547; AAC50508.1; -
DR EMBL; BC016174; AAH16174.1; -
DR EMBL; BC028578; AAH28578.1; -
DR PIR; S68450; S68450.
DR PDB; 1QBH; 20-OCT-99.
DR Genew; HGNC:590; BIRC2.
DR MIM; 601712; -
DR GO; GO:0008189; P:apoptosis inhibitor activity; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS01433; BIR_REPEAT_2; 3.
DR PROSITE; PS02029; CARD; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR AP00089; Zinc-finger; Repeat; 3D-structure.
FT REPEAT 46 113
FT REPEAT 184 250
FT REPEAT 269 336
FT DOMAIN 453 543
FT ZN_FING 571 606
FT CONFLICT 157 157 S -> P (IN REF. 2).
FT CONFLICT 308 308 C -> G (IN REF. 2).
FT CONFLICT 414 414 Q -> L (IN REF. 2).
FT CONFLICT 514 514 L -> W (IN REF. 2).
FT TURN 269 270
FT HELIX 271 274
FT HELIX 287 293
FT TURN 294 294
FT TURN 296 297
FT TURN 301 304
FT STRAND 309 309
FT HELIX 322 325
FT TURN 326 328
FT STRAND 333 333
FT TURN 334 343
FT HELIX 344 351
FT TURN 353 354
SQ SEQUENCE 618 AA; 69899 MW; C1778D328063586D CRC64;

Query Match 47.4%; Score 183; DB 1; Length 618;
Best Local Similarity 51.5%; Pred. No. 3.1e-14;
Matches 35; Conservative 9; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARTVPTGWIYS--VNKEQLAAGFYALGEGDKVKCFHCGGLTDWKPSPDPNDQAK 58
DB 269 HAARWTFWYWPSSVPVQPEQLASAGFYVGRNDVVKCFCCDGLRCWESGDDPWVEHAK 328
QY 59 CYPGCKYL 66
DB 329 WFFRCFPL 336

RESULT 14
ID IAP1_DROME STANDARD; PRT; 438 AA.
AC Q24306;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Apoptosis 1 inhibitor (inhibitor of apoptosis 1) (DIAP1) (Thread Protein).
```

```
GN IAP1 OR TH.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Eye imaginal disk;
RX MEDLINE=96128128; PubMed=8548811;
RA Hay B.A., Wassarman D.A., Rubin G.M.;
RT Drosophila homologs of baculovirus inhibitor of apoptosis proteins function to block cell death.;
RL Cell 83:1253-1262(1995).
CC -!- FUNCTION: APOPTOTIC SUPPRESSOR. OVEREXPRESSION SUPPRESSES RPR AND -!- FUNCTION: APOPTOTIC CELL DEATH IN THE EYE.
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 2 BIR repeats.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
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CC EMBL; L49440; AAC41609.1; -
DR PDB; 1JD4; 05-DEC-01.
DR PDB; 1JD5; 05-DEC-01.
DR PDB; 1JD6; 05-DEC-01.
DR FlyBase; FBgn0003691; th.
DR GO; GO:0008189; P:apoptosis inhibitor activity; IDA.
DR GO; GO:0006916; P:anti-apoptosis; IDA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 2.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 2.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS01433; BIR_REPEAT_2; 2.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR AP00089; Zinc-finger; Repeat; 3D-structure.
FT REPEAT 44 110
FT REPEAT 226 293
FT ZN_FING 391 426 RING-TYPE
SQ SEQUENCE 438 AA; 48098 MW; A6C22C8EDF5AEF29 CRC64;

Query Match 46.1%; Score 178; DB 1; Length 438;
Best Local Similarity 45.5%; Pred. No. 8.8e-14;
Matches 30; Conservative 15; Mismatches 19; Indels 2; Gaps 1;

QY 3 ARIVTGTWIVSNKE--QLASAGFYALGEGDKVKCFHCGGLTDWKPSPDPNDQAKCY 60
DB 228 ARLTFTFAPRNLLKQPHQLAAGFYTGVRVRCFCGCGGLMDNDNDEPWEQHALWL 287
QY 61 PGCKYL 66
DB 288 SQCRFV 293

RESULT 15
ID BIR7_HUMAN STANDARD; PRT; 298 AA.
AC Q95CAs; Q9BOV0; Q9H2A8; Q9HAP7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Baculoviral IAP repeat-containing protein 7 (Kidney inhibitor of apoptosis protein) (KIAP) (Melanoma inhibitor of apoptosis protein).
```

DE (ML-IAP) (Livin).
GN BIRC7 OR KIAIP OR ML-IAP OR LIVIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RP TISSUE=Fetal Kidney;
RX MEDLINE=21092523; PubMed=11162435;
RA Lin J.-H., Deng G., Huang Q., Morser J.;
RT "KIAIP, a novel member of the inhibitor of apoptosis protein family.";
RL Biochem. Biophys. Res. Commun. 279:820-831(2000).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RP TISSUE=Melanoma;
RX MEDLINE=2123043; PubMed=11322947;
RA Ashhab Y., Allian A., Polliack A., Panet A., Yehuda D.B.;
RT "Two splicing variants of a new inhibitor of apoptosis gene with
RT different biological properties and tissue distribution pattern.";
RL FEBS Lett. 495:56-60(2001).
RN [3]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Kidney;
RX PubMed=11024045;
RA Kasof G.M., Gomes B.C.;
RT "Livin, a novel inhibitor of apoptosis protein family member.";
RL J. Biol. Chem. 276:3238-3246(2001).
RN [4]
RN SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RP MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahm D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaeslaitho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.I., Martin S.I., McConachie L.J., McKay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.W., Ross M.T., Scott C.B., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.D., Soderlund C., Steward C.A., Sutcliffe J.B.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [5]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RP TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madañ A., Rodrigues S., Sanchez A.,
RA Whiting M., Madañ A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RN FUNCTION, AND MUTAGENESIS OF GLU-87; GLU-88; CYS-124; ASP-120 AND
RP ASP-138.
RX MEDLINE=20538921; PubMed=11084335;
RA Vucic D., Stennicke H.R., Pisabarro M.T., Salvesen G.S., Dixit V.M.;
RT "ML-IAP, a novel inhibitor of apoptosis that is preferentially
RT expressed in human melanomas.";
RL Curr. Biol. 10:1359-1366(2000).
RN [7]
RN INTERACTION WITH SMAC.
RX MEDLINE=21922807; PubMed=11801603;
RA Vucic D., Deshayes K., Ackery H., Pisabarro M.T., Kadkhodayan S.,
RA Fairbrother W.J., Dixit V.M.;
RT "SMAC negatively regulates the anti-apoptotic activity of melanoma
RT inhibitor of apoptosis (ML-IAP).";
RL J. Biol. Chem. 277:12275-12279(2002).
RN [8]
RN ACTIVATION OF MAP KINASES.
RX MEDLINE=21853687; PubMed=11865055;
RA Sanna M.G., da Silva Correia J., Ducrey O., Lee J., Nomoto K.,
RA Schrantz N., Deveraux Q.L., Ulevitch R.J.;
RT "IAP suppression of apoptosis involves distinct mechanisms: the
RT TAK1/JNK1 signaling cascade and caspase inhibition.";
RL Mol. Cell. Biol. 22:1754-1766(2002).
RN [9]
RN FUNCTION: Protects against apoptosis induced by TNF or by chemical
RN agents such as adriamycin, etoposide or staurosporine. Suppression
RN of apoptosis is mediated by activation of MAPK8/JNK1, and possibly
RN also of TAK1/JNK2. This activation depends on TAB1 and
RN NR2C2/PAK1. In vitro, inhibits caspase-3 and proteolytic
RN activation of pro-caspase-9. Isoform 1 blocks staurosporine-
RN induced apoptosis and isoform 2 blocks etoposide-induced
RN apoptosis.
RN [10]
RN SUBUNIT: Binds to caspase-9. Interaction with SMAC via the BIR
RN domain disrupts binding to caspase-9 and apoptotic suppressor
RN activity. Interacts with TAB1. In vitro, interacts with caspase-3
RN and caspase-7 via its BIR domain.
RN [11]
RN SUBCELLULAR LOCATION: Nuclear, and in a filamentous pattern
RN throughout the cytoplasm.
RN [12]
RN ALTERNATIVE PRODUCTS:
RN Event=Alternative splicing; Named isoforms=3;
RN Name=2; Synonyms=Livin alpha;
RN IsoId=Q96CA5-1; Sequence=Displayed;
RN Name=1; Synonyms=Livin beta;
RN IsoId=Q96CA5-2; Sequence=VSP_002459;
RN Name=3;
RN IsoId=Q96CA5-3; Sequence=VSP_002458;
RN [13]
RN TISSUE SPECIFICITY: Very low levels or not detectable in most
RN adult tissues. Detected in adult heart, placenta, lung, lymph
RN node, spleen and ovary, and in several carcinoma cell lines
RN (isoforms 1 and 2). Isoform 2 (but not isoform 1) is detected in
RN fetal kidney, heart and spleen, and at lower levels in adult
RN brain, skeletal muscle and peripheral blood leukocytes.
RN [14]
RN SIMILARITY: Belongs to the IAP family.
RN [15]
RN SIMILARITY: Contains 1 BIR repeat.
RN [16]
RN SIMILARITY: Contains 1 RING-type zinc finger.
RN [17]
RN This SWISS-PROT entry is copyright. It is produced through a collaboration
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Search completed: March 10, 2004, 13:53:00
Job time : 11.5 secs

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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:48:59 ; Search time 36 Seconds
(without alignments)
578.450 Million cell updates/sec

Title: US-09-654-743-24

Perfect score: 386

Sequence: 1 YEARIIVFGTWISVNKEQL.....KPSDDPDQHXKCYPCCKYL 66

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	366	94.8	Q9EF0	Q9EF0 rattus norv
2	366	94.8	Q9EQ04	Q9EQ04 rattus norv
3	361	93.5	Q9EQ05	Q9EQ05 rattus norv
4	306	79.3	Q9ERW6	Q9ERW6 homo sapien
5	279	72.3	Q9UVP8	Q9UVP8 gallus gall
6	258	66.8	Q8WMY4	Q8WMY4 bos taurus
7	212	54.9	Q8UWH2	Q8UWH2 brachydanio
8	212	54.9	Q7SXU1	Q7SXU1 brachydanio
9	192	49.7	Q9IA70	Q9IA70 gallus gall
10	192	49.7	Q9IA69	Q9IA69 gallus gall
11	192	49.7	Q9IES9	Q9IES9 rattus norv
12	192	49.7	Q921N0	Q921N0 gallus gall
13	189	49.0	Q921N0	Q921N0 mus musculus
14	189	49.0	Q804E2	Q804E2 ictalurus p
15	189	49.0	Q8UWD2	Q8UWD2 brachydanio
16	189	49.0	Q7T0K2	Q7T0K2 brachydanio

17	185	47.9	346	5	Q969T8	Q969T8 bombyx mori
18	185	47.9	346	5	Q8IS31	Q8IS31 bombyx mori
19	185	47.9	589	11	Q9Q2C6	Q9Q2C6 rattus norv
20	185	47.9	589	11	Q9ESE8	Q9ESE8 rattus norv
21	183	47.4	534	4	Q8I2Z0	Q8I2Z0 homo sapien
22	180	46.6	263	12	Q8OSF4	Q8OSF4 hyphantria
23	180	46.6	283	12	Q80LK8	Q80LK8 adxophyes
24	180	46.6	403	5	Q8MRD9	Q8MRD9 aedes trise
25	178	46.1	438	5	Q9VUX5	Q9VUX5 drosophila
26	177	45.9	261	12	Q9QES9	Q9QES9 epiphyas po
27	177	45.9	264	12	Q9EN27	Q9EN27 amsacta moo
28	177	45.9	379	5	Q9U492	Q9U492 trichoplusi
29	176	45.6	377	5	Q9NJ07	Q9NJ07 spodoptera
30	175	45.3	401	13	Q8JHV9	Q8JHV9 xenopus lae
31	173	44.8	255	12	Q7T5S1	Q7T5S1 cryptophleb
32	173	44.8	324	13	Q9DDN2	Q9DDN2 gallus gall
33	171	44.3	281	12	Q9DNL8	Q9DNL8 choristoneu
34	170	44.0	402	5	Q8T621	Q8T621 aedes albop
35	167	43.3	213	5	Q8MVN1	Q8MVN1 boltenia vl
36	164.5	42.6	276	12	Q89744	Q89744 buzura supp
37	164.5	42.6	1403	11	Q8CH68	Q8CH68 mus musculu
38	164.5	42.6	1403	11	Q8CH64	Q8CH64 mus musculu
39	163.5	42.4	597	11	Q9R015	Q9R015 mus musculu
40	163.5	42.4	1402	11	Q8CH65	Q8CH65 mus musculu
41	163.5	42.4	1402	11	Q8CGT4	Q8CGT4 mus musculu
42	163.5	42.4	1402	11	Q8CGT3	Q8CGT3 mus musculu
43	163.5	42.4	1403	11	Q8CH70	Q8CH70 mus musculu
44	163.5	42.4	1403	11	Q8CGT2	Q8CGT2 mus musculu
45	163.5	42.4	1403	11	Q8BG68	Q8BG68 mus musculu

ALIGNMENTS

RESULT 1

Q9ESF0 PRELIMINARY; PRT; 496 AA.

AC Q9ESF0; ID Q9ESF0; AC Q9ESF0; DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF183429; AAG22969.1; -.
DR HSSP; P98170; 1G3F.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008193; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR REPEAT 1; 3.
DR PROSITE; PS0143; BIR REPEAT 2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 496 AA; 56117 MW; 9BEF142AAEC5B798 CRC64;

Query Match 94.8%; Score 366; DB 11; Length 496;
Best Local Similarity 93.9%; Pred. No. 5.9e-35;
Matches 62; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 YEARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPDQHAQY 60
Db 264 YDARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPDQHAQY 323

Qy 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 2
Q9EQ04 PRELIMINARY; PRT; 501 AA.
AC Q9EQ04;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Ovary;
RA Lareu R.R., Bradley C.K., Lacher M., Friis R.R., Dharmarajan A.M.;
RT "Cloning, characterization and regulation of an inhibitor of apoptosis
protein in the rat corpus luteum";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 501 AA; 56578 MW; 4863F5F2F2E0C8CD CRC64;

Query Match 94.8%; Score 366; DB 11; Length 501;
Best Local Similarity 93.9%; Pred. No. 5.9e-35;
Matches 62; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YEARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPDQHAQY 60
Db 264 YDARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPDQHAQY 323

Qy 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 3
Q9EQ05 PRELIMINARY; PRT; 501 AA.
AC Q9EQ05;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Ovary;
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RA Lareu R.R., Bradley C.K., Lacher M., Friis R.R., Dharmarajan A.M.;
RT "Cloning, characterization and regulation of an inhibitor of apoptosis
protein in the rat corpus luteum";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 501 AA; 56548 MW; 0973FBF2B8E1C5A0 CRC64;

Query Match 93.5%; Score 361; DB 11; Length 501;
Best Local Similarity 92.4%; Pred. No. 2.3e-34;
Matches 61; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YEARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPDQHAQY 60
Db 264 YDARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPDQHAQY 323

Qy 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 4
Q96RW6 PRELIMINARY; PRT; 106 AA.
AC Q96RW6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE IAP-like protein 3.
OS ILP3.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mir S.S., Duckett C.S.;
RT "Molecular cloning of human homologs of IAP-like protein.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF164681; AAK81891.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 106 AA; 12360 MW; 6B8AD3A8A80A891 CRC64;

Query Match 79.3%; Score 306; DB 4; Length 106;
Best Local Similarity 91.1%; Pred. No. 1.4e-28;
Matches 51; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 11 WIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPDQHAQYPCCKYL 66
Db 2 WIYSVNKEQLSRAGFYALGEGDKVKCFHCGGGLTDWKPSEDPDQHAQYPCCKYL 57

RESULT 5
Q8UVF8
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ID Q8UVF8 PRELIMINARY; PRT; 493 AA.
AC Q8UVF8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 3.
GN IAP3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Brigham J.T., Johnson A.L.;
RT "Identification of chicken inhibitor of apoptosis protein XIAP
(IAP3).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF451854; AAL47170.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 493 AA; 55251 MW; 030A9F56CB6119BC CRC64;
Query Match 72.3%; Score 279; DB 13; Length 493;
Best Local Similarity 71.2%; Pred. No. 1.2e-24;
Matches 47; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
QY 1 YEARIIVTGTWYISVNVKQLARAGFYALGEGDKVKCFHCGGLTDWKPSPEDPDQAKY 60
DB 264 YERRIQTFLAWITPVNKEHLAERGFYSTGNGDHVYVCFHCGGLQEWKENSDPDQAKWF 323
QY 61 PGCKYL 66
DB 324 PGCKFL 329
RESULT 6
Q8WVY4 PRELIMINARY; PRT; 109 AA.
AC Q8WVY4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE X-linked inhibitor of apoptosis protein (Fragment).
GN XIAP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Gutierrez-Adan A., Madrid-Bury N., Arroyo-Garcia R., Fernandez R.,
RA Jimenez A., Pintado B., De la Fuente J.;
RT "Hypoglycemia-induced apoptosis affects sex ratio of preimplantation
embryos.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF458770; AAL6179.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.

InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1 109
SQ SEQUENCE 109 AA; 12361 MW; C4027DC88213DE6D CRC64;
Query Match 66.8%; Score 258; DB 6; Length 109;
Best Local Similarity 91.7%; Pred. No. 7.2e-23;
Matches 44; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 YEARIIVTGTWYISVNVKQLARAGFYALGEGDKVKCFHCGGLTDWKP 48
DB 57 YEARIITFTWYISVNVKQLARAGFYALGEGDKVKCFHCGGLNDWKP 104
RESULT 7
Q8UWH2 PRELIMINARY; PRT; 405 AA.
ID Q8UWH2
AC Q8UWH2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Xiap.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
zebrafish.";
RL Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF439767; AAL32047.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 405 AA; 45564 MW; A366E342D83BECAB CRC64;
Query Match 54.9%; Score 212; DB 13; Length 405;
Best Local Similarity 51.5%; Pred. No. 8.6e-17;
Matches 34; Conservative 14; Mismatches 18; Indels 0; Gaps 0;
QY 1 YEARIIVTGTWYISVNVKQLARAGFYALGEGDKVKCFHCGGLTDWKPSPEDPDQAKY 60
DB 229 FEGSLDFKGRQHPIDPERLARAGFYSTGEQDRVMCFRCGGVAKWMPDEDPWEHARHY 288
QY 61 PGCKYL 66
DB 289 PGCSFL 294
RESULT 8
Q7SXU1 PRELIMINARY; PRT; 415 AA.
ID Q7SXU1

[illegible]

```
Db 117 HEARVKTFINWPTIPVQPEQLADAGFYVYGRNDVYKFCFCCDGLRCWESGDDPWIEHAK 176
QY 59 CYPCKYL 66
Db 177 WFPCEYL 184

RESULT 11
Q9SE9 PRELIMINARY; PRT; 602 AA.
AC Q9SE9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE Inhibitor of apoptosis protein 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP "Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF183430; AAG22970.1; -.
DR HSP; Q13490; 1QBH.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00653; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS01282; BIR_REPEAT_2; 3.
DR PROSITE; PS0143; BIR_REPEAT_1; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 602 AA; 67326 MW; CC91385EEA62DE5A CRC64;

Query Match 49.7%; Score 192; DB 11; Length 602;
Best Local Similarity 51.5%; Pred. No. 3.1e-14;
Matches 35; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIIVFTGIWYS--VYKQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPDWQHAK 58
Db 255 HAARVTFSTWPSALVHPQELASAGFYTGHSDDVKFCFCCDGLRCWESGDDPWIEHAK 314
QY 59 CYPCKYL 66
Db 315 WFPCEYL 322

RESULT 12
O57319 PRELIMINARY; PRT; 610 AA.
AC O57319;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE Inhibitor of apoptosis protein 1 (IAP) (Inhibitor of T cell apoptosis
DE PROTEINE).
GN IAP1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEHORN; TISSUE=EMERYONIC FIBROBLAST;
RX MEDLINE=98038801; PubMed=9372964;
RA You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;
RT "ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a
RL mediator of the antiapoptotic activity of the v-rel oncoprotein.";
MOl. Cell. Biol. 17:7328-7341(1997).
CC -1- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED
CC CELLS.
CC -1- SUBCELLULAR LOCATION: EXPRESSED PREDOMINANTLY IN THE CYTOPLASM OF
CC THE V-REL-TRANSFORMED CELLS.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN THE
CC SPLEEN, THYMUS, BURS, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS
CC IN TESTIS, BRAIN, AND SKELETAL MUSCLE.
CC -1- INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION
CC PROCESS.
CC -1- DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC EFFECT.
CC -1- SIMILARITY: MEMBER OF THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION OF
CC APOPTOSIS PROTEIN REPEAT).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL; AF008592; AAB88044.1; -.
DR HSP; Q13490; 1QBH.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00653; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS01282; BIR_REPEAT_2; 3.
DR PROSITE; PS0143; BIR_REPEAT_1; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 30 97 BIR_REPEAT_1.
FT REPEAT 176 242 BIR_REPEAT_2.
FT REPEAT 262 329 BIR_REPEAT_3.
FT ZN FING 563 597 C3HC4-TYPE.
SQ SEQUENCE 610 AA; 68924 MW; ADF47619650B44A6 CRC64;

Query Match 49.7%; Score 192; DB 13; Length 610;
Best Local Similarity 52.9%; Pred. No. 3.2e-14;
Matches 36; Conservative 8; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIIVFTGTW--IYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPDWQHAK 58
Db 262 HEARVKTFINWPTIPVQPEQLADAGFYVYGRNDVYKFCFCCDGLRCWESGDDPWIEHAK 321
QY 59 CYPCKYL 66
Db 322 WFPCEYL 329

RESULT 13
Q921NO PRELIMINARY; PRT; 374 AA.
AC Q921NO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Inhibitor of apoptosis protein 1 (IAP) (Inhibitor of T cell apoptosis
DE PROTEINE).
GN IAP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```


OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC011338; AAH11338.1; -.
DR MGD; MGI:1197007; Birc2.

DR GO; GO:0005622; C:intracellular; IEA.

DR GO; GO:000189; F:apoptosis inhibitor activity; IEA.

DR GO; GO:0006916; P:anti-apoptosis; IEA.

DR InterPro; IPR001370; BIR.

DR SMART; PF00653; BIR; 3.

DR GO; GO:000238; BIR; 3.

DR PROSITE; PS01282; BIR_REPEAT_1; 3.

DR PROSITE; PS0143; BIR_REPEAT_2; 3.

SQ SEQUENCE 374 AA; 41915 MW; 1D2B54C3D2D7E46F3 CRC64;

Query Match 49.0%; Score 189; DB 11; Length 374;

Best Local Similarity 51.5%; Pred. No. 4.2e-14;

Matches 35; Conservative 9; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARTVFTGWTYS--VNKEQLARAGFYALGSDVKVCFHCGGLTDWKPSDDPDQHAH 58

DB 253 HAARTFTFNWPSALVHSELASAGFYTGHSDDVKVCFCDGGLRCWESGDDPDVVEHAK 312

QY 59 CYPCKYL 66

DB 313 WPRCEYL 320

RESULT 14

Q804E2 PRELIMINARY; PRT; 616 AA.

AC Q804E2;

DT 01-JUN-2003 (T-EMBLrel. 24, Created)

DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Inhibitor of apoptosis protein-1.

GN CTAP-1.

OS Ictalurus punctatus (Channel catfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Siluriformes;

OC Ictaluridae; Ictalurus.

OX NCBI_TaxID=7998;

RN [1]

RP SEQUENCE FROM N.A.

RA Praveen K., Leary J.H. III, Evans D.L., Jaso-Friedmann L.;

RT "Cloning of anti-apoptotic genes in non-specific cytotoxic cells."

RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY184377; AAC24632.1; -.

DR GO; GO:0005622; C:intracellular; IEA.

DR GO; GO:000189; F:apoptosis inhibitor activity; IEA.

DR GO; GO:0006916; P:anti-apoptosis; IEA.

DR InterPro; IPR001370; BIR.

DR InterPro; IPR001315; CARD.

DR InterPro; IPR001841; Znf_ring.

DR Pfam; PF00653; BIR; 3.

DR Pfam; PF00619; CARD; 1.

DR SMART; SM00238; BIR; 3.

DR SMART; SM00114; CARD; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01282; BIR_REPEAT_1; 2.

DR PROSITE; PS0143; BIR_REPEAT_2; 3.

DR PROSITE; PS0209; CARD; 1.

DR PROSITE; PS0089; ZF_RING_2; 1.

SQ SEQUENCE 616 AA; 69546 MW; DL389D915C6B256 CRC64;

Query Match

Best Local Similarity 49.0%; Score 189; DB 13; Length 616;

Matches 34; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

QY 2 EARIVTFGTW--IYSVNKEQLARAGFYALGSDVKVCFHCGGLTDWKPSDDPDQHAH 59

DB 270 EERLLTFVNWPARIPVRPDQLAKAGFYVVGRRDDVKVCFCDGGLRCWESGDDPDVVEHAKW 329

QY 60 YPCKYL 66

DB 330 FPRCEYL 336

RESULT 15

Q8UWD2 PRELIMINARY; PRT; 628 AA.

AC Q8UWD2;

DT 01-MAR-2002 (T-EMBLrel. 20, Created)

DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

DE IAP1.

GN IAP1.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-20373792; PubMed=10917738;

RT "Genes with homology to mammalian apoptosis regulators identified in

zebrafish."

RL Cell Death Differ. 7:509-510(2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Inohara N., Nunez G.;

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

DR EMBL; AF442500; AAL33679.1; -.

DR GO; GO:0005622; C:intracellular; IEA.

DR GO; GO:000189; F:apoptosis inhibitor activity; IEA.

DR GO; GO:0006916; P:anti-apoptosis; IEA.

DR InterPro; IPR001370; BIR.

DR InterPro; IPR001315; CARD.

DR InterPro; IPR001841; Znf_ring.

DR Pfam; PF00653; BIR; 3.

DR Pfam; PF00619; CARD; 1.

DR SMART; SM00238; BIR; 3.

DR SMART; SM00114; CARD; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01282; BIR_REPEAT_1; 2.

DR PROSITE; PS0143; BIR_REPEAT_2; 3.

DR PROSITE; PS0209; CARD; 1.

DR PROSITE; PS0089; ZF_RING_2; 1.

KW Metal-binding; Zinc; Zinc-finger.

SQ SEQUENCE 628 AA; 70098 MW; 5B68CEB6A87C8A95 CRC64;

Query Match 49.0%; Score 189; DB 13; Length 628;

Best Local Similarity 50.7%; Pred. No. 7.5e-14;

Matches 34; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

QY 2 EARIVTFGTW--IYSVNKEQLARAGFYALGSDVKVCFHCGGLTDWKPSDDPDQHAH 59

DB 280 EERLLTFVNWPSRIPVRPDQLAKAGFYVVGRRDDVKVCFCDGGLRCWESGDDPDVVEHAKW 339

QY 60 YPCKYL 66

DB 340 FPRCEYL 346

Search completed: March 10, 2004, 13:54:25

Job time : 37 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:42:09 ; Search time 49.5 Seconds
(without alignments)
376.730 Million cell updates/sec

Title: US-09-654-743-25

Perfect score: 389

Sequence: 1 YEARIFTFTWTIYVNKEQL.....KPSDEPWEQFAKWYPCCKYL 66

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.GeneSeq_29Jan04:*
1: GeneSeqp1980s.*
2: GeneSeqp1980s.*
3: GeneSeqp2000s.*
4: GeneSeqp2001s.*
5: GeneSeqp2002s.*
6: GeneSeqp2003as.*
7: GeneSeqp2003bs.*
8: GeneSeqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	389	100.0	66	7 ADB61810	ADB61810 Human inh
2	389	100.0	236	5 ABG32418	ABG32418 X-linked
3	389	100.0	278	5 AAO20511	AAO20511 Protein o
4	389	100.0	497	2 AAW19581	AAW19581 Human apo
5	389	100.0	497	2 AAW69294	AAW69294 Human XIA
6	389	100.0	497	3 AAY59451	AAY59451 Human XIA
7	389	100.0	497	3 AAY99985	AAY99985 Human X-1
8	389	100.0	497	5 ABG56663	ABG56663 Human inh
9	389	100.0	497	7 ADB80961	ADB80961 RING-SH c
10	377	96.9	66	7 ADB61827	ADB61827 Rat inhib
11	368	94.6	496	2 AAW19745	AAW19745 Mouse inh
12	366	94.1	496	2 AAW19584	AAW19584 Mouse apo
13	366	94.1	496	2 AAW9297	AAW9297 Murine XI
14	366	94.1	496	5 ABG56666	ABG56666 Mouse inh
15	352	90.5	66	7 ADB61828	ADB61828 Mouse inh
16	352	90.5	496	6 ABP72157	ABP72157 Mouse inh
17	347	89.2	66	7 ADB61820	ADB61820 Human inh
18	347	89.2	236	3 AAY81440	AAY81440 Human XIA
19	347	89.2	236	4 AAE00365	AAE00365 Human IAP
20	347	89.2	236	5 AAU75066	AAU75066 Human tes
21	347	89.2	236	5 ABG32417	ABG32417 Inhibitor
22	347	89.2	464	5 AAU75747	AAU75747 Human inh
23	341	87.7	236	4 AAE00366	AAE00366 Chimpanzee
24	338	86.9	66	7 ADB61831	ADB61831 Gorilla i
25	338	86.9	236	4 AAE00367	AAE00367 Gorilla I

26	322	82.8	57	7 ADB61832	ADB61832 Unidentif
27	287	73.8	66	7 ADB61829	ADB61829 Chicken i
28	255	65.6	52	7 ADB61830	ADB61830 Bovine inh
29	216	55.5	68	7 ADB61833	ADB61833 Zebra fis
30	211	54.2	68	7 ADB61813	ADB61813 Human inh
31	211	54.2	557	6 ABP72159	ABP72159 Inhibitor
32	211	54.2	604	2 AAW19582	AAW19582 Human apo
33	211	54.2	604	2 AAW19747	AAW19747 Human inh
34	211	54.2	604	2 AAW13546	AAW13546 Human c-I
35	211	54.2	604	2 AAW69295	AAW69295 Human HIA
36	211	54.2	604	2 AAY52703	AAY52703 Human cel
37	211	54.2	604	2 AAY33997	AAY33997 Human cel
38	211	54.2	604	5 ABG56664	ABG56664 Human inh
39	211	54.2	604	6 ABU07431	ABU07431 Protein d
40	211	54.2	604	6 ABB82739	ABB82739 Human CIA
41	211	54.2	604	7 ADB80948	ADB80948 RING-SH c
42	211	54.2	604	7 AAE39811	AAE39811 Human cel
43	211	54.2	1140	5 AAU97837	AAU97837 Human cys
44	211	54.2	1141	4 AAB50694	AAB50694 Human API
45	203	52.2	600	2 AAW69298	AAW69298 Murine HI

ALIGNMENTS

RESULT 1

ADB61810
ID ADB61810 standard; protein; 66 AA.

XX AC ADB61810;

XX DT 04-DEC-2003 (first entry)

XX DE Human inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.

XX KW baculovirus inhibitor of apoptosis repeat domain; BIR domain;

KW apoptosis pathway; embryonic development; viral pathogenesis; cancer;

KW autoimmune disorder; neurodegenerative disease; apoptotic response;

KW systemic lupus erythematosus; multiple sclerosis; viral infection;

KW herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;

KW HAP1; CIAP2; HIA2; CIAP1; RING zinc finger; caspase-3; caspase-7;

KW caspase-9; cytostatic; neoplasm; leukaemia; colon carcinoma;

KW cervical cancer; uterine cancer; testicular cancer;

KW small cell lung carcinoma; uterine cancer; renal cell carcinoma;

KW Wilm's tumour; human; BIR 3 domain.

XX OS Homo sapiens.

XX FN WO2003040172-A2

XX PD 15-MAY-2003.

XX PF 12-NOV-2002; 2002WO-CA001738.

XX PR 09-NOV-2001; 2001US-0332300P.

XX FR 08-APR-2002; 2002US-0370934P.

XX PA (ABGE-) AEGERA THERAPEUTICS INC.

XX FI Boudreault A, Korneluk RG, La Casse E, Liston P;

XX DR WPI; 2003-513532/48.

XX PT Polypeptide capable of forming a complex with a polypeptide comprising a

PT baculovirus inhibitor of apoptosis repeat domain useful for treating

PT cancer and other neoplasms.

XX ES Disclosure; Fig 1A; 53pp; English.

XX CC This invention relates to a substantially pure polypeptide having a

CC length of less than 100 amino acids and capable of forming a complex with

CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat

CC (BIR) domain. The apoptosis pathway is known to play a critical role in

CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
CC and neurodegenerative diseases. The failure of the apoptotic response has
CC been implicated in the development of cancer, autoimmune disorders (for
CC example systemic lupus erythematosus and multiple sclerosis) and viral
CC infections (including herpes virus, poxvirus and adenovirus). The
CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HRAPI
CC (CIAP2) and HRAPI2 (CIAP1) all possess three BIR domains and carboxy
CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
CC -9 which are proteases involved in the initiation of apoptosis. Compounds
CC which inhibit the activity of IAPs may therefore have cytostatic activity
CC through the enhancement of apoptosis. The polypeptides of the invention
CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
CC may be useful for the treatment of cancer and other neoplasms, such as
CC leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
CC and Wilm's tumour, and for enhancing apoptosis. The present sequence is
CC that of the human inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
CC against which the peptides of the invention are targeted to bind.

XX
SQ Sequence 66 AA;

Query Match 100.0%; Score 389; DB 7; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.3e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIPTFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDEDPWEQHAQWY 60

DB 1 YEARIPTFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDEDPWEQHAQWY 60

QY 61 PGCKYL 66

DB 61 PGCKYL 66

RESULT 2

ID ABG32418

AC ABG32418 standard; protein; 236 AA.

XX
AC ABG32418;

XX
DT 15-NOV-2002 (first entry)

XX
DE X-linked inhibitor of apoptosis protein, XIAP.

XX
DE Inhibitor of apoptosis protein; IAP; testis; XIAP; apoptosis; inhibitor;

XX
KW fertility; testicular cancer; male infertility; male birth control;

XX
KW X-linked inhibitor of apoptosis protein; XIAP.

XX
OS Mammalia.

XX
FH Key Location/Qualifiers

XX
FT Misc-difference 1

XX
FT /note= "Encoded by nnn; start codon is illegible in

XX
FT specification"

XX
FN US2002086409-A1.

XX
PD 04-JUL-2002.

XX
PF 18-DEC-2001; 2001US-00024433.

XX
PR 29-JAN-1998; 98US-0073001P.

XX
PR 29-JAN-1999; 99US-00239867.

XX
XX (KORN/) KORNELUK R G.

XX
PA (LAGA/) LAGACE M.

XX
XX Korneluk RG, Lagace M;

XX
XX WPI; 2002-642245/69.

XX
XX N-PSDB; ABS52803.

XX
XX

PT Novel polypeptide, a member of inhibitor of apoptosis family of proteins
PT that is expressed in testes useful for modulating apoptosis in cells,
PT particular cells involved in male fertility.

XX
XX Example 3; Fig 4B; 24pp; English.

XX
CC A substantially pure TIAP polypeptide (I), a member of IAP (inhibitor of
CC apoptosis) family of proteins that is expressed in the testes. (I) is
CC useful for identifying a compound that modulates TIAP biological activity
CC (I) is useful for increasing apoptosis in a cell, preferably a germ-line
CC cell and for increasing fertility in an animal. (I) is useful for
CC treating or preventing apoptosis which occurs as a part of testicular
CC cancer and male infertility. TIAP may be manipulated for use as a male
CC birth control. TIAP polypeptides and nucleic acid sequences also have
CC diagnostic use in the detection or monitoring of conditions involving
CC aberrant levels of apoptosis. The present sequence represents the amino
CC acid sequence of X-linked inhibitor of apoptosis protein, XIAP

XX
SQ Sequence 236 AA;

Query Match 100.0%; Score 389; DB 5; Length 236;

Best Local Similarity 100.0%; Pred. No. 5.5e-39;

Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIPTFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDEDPWEQHAQWY 60

DB 4 YEARIPTFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDEDPWEQHAQWY 63

QY 61 PGCKYL 66

DB 64 PGCKYL 69

RESULT 3

AAO20511

ID AAO20511 standard; protein; 278 AA.

XX
AC AAO20511;

XX
DT 27-JUN-2002 (first entry)

XX
DE Protein of APP related human homologue hCP35211.

XX
XX Neuroprotective; nontropic; transgenic fly; Alzheimer's disease; Abeta;

XX
KW amyloid precursor protein; tissue-specific expression control; human APP;

XX
KW APP pathway modulator; gene therapy.

XX
OS Homo sapiens.

XX
PN WO200226820-A2.

XX
PD 04-APR-2002.

XX
PF 01-OCT-2001; 2001WO-EP011345.

XX
XX 29-SEP-2000; 2000US-0236893P.

XX
PR 14-JUN-2001; 2001US-0298309P.

XX
XX (NOVS) NOVARTIS AG.

XX
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX
XX Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;

XX
PI Reinhardt MWHM, Zusman S;

XX
XX WPI; 2002-315796/35.

XX
DR N-PSDB; AAK99405.

XX
XX New transgenic fly, containing DNA encoding an Abeta portion of human

XX
PT APP, useful for identifying agents which modulate the APP pathway and

XX
PT which can be used to treat Alzheimer's disease.

XX
XX Example 4; Page 112; 129pp; English.

XX
XX

CC The invention relates to a transgenic fly whose genome comprises DNA
 CC encoding a polypeptide having the Abeta portion of human amyloid
 CC precursor protein (APP), fused to a signal sequence. The DNA sequence
 CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
 CC the specification. The DNA sequence is operably linked to a tissue-
 CC specific expression control sequence. Expression of the sequence gives
 CC the fly an altered phenotype. The purpose of the invention is for
 CC identifying agents that inhibit or promote the expression and/or function
 CC of genes or encoded polypeptides which modify the APP pathway. The agent
 CC is a compound, triple helix DNA, antisense oligonucleotide, double
 CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used
 CC to treat conditions such as Alzheimer's disease. The agent can be used as
 CC an APP pathway modulator or in gene therapy. This sequence represents the
 CC protein of the APP related human homologue hCP35211
 XX
 SQ Sequence 278 AA;

Query Match 100.0%; Score 389; DB 5; Length 278;
 Best Local Similarity 100.0%; Pred. No. 6.7e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPEQHAQWY 60
 DB 46 YEARIFTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPEQHAQWY 105
 QY 61 PGCKYL 66
 DB 106 PGCKYL 111

RESULT 4
 AA19581
 XX ID AA19581 standard; protein; 497 AA.
 AC AA19581;
 XX
 DT 02-SEP-1997 (first entry)
 DE Human apoptosis inhibitor XIAP.

XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; XIAP; HIV;
 KW AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia;
 KW myocardial infarction; stroke; reperfusion injury;
 KW toxin-induced liver disease; gene therapy; diagnosis.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Domain 26..93
 FT /label= BIR-1
 FT Domain 163..230
 FT /label= BIR-2
 FT Domain 265..330
 FT /label= BIR-3
 FT Domain 439..484
 FT /label= Ring_zinc_finger

XX WO9706255-A2.
 XX
 XX 20-FEB-1997.
 XX
 XX 05-AUG-1996; 96WO-IB001022.
 XX
 XX 04-AUG-1995; 95US-00511485.
 PR 22-DEC-1995; 95US-00576956.
 XX
 XX (UYOT-) UNIV OTTAWA.

XX Korneluk RG, Mackenzie AE, Baird S, Liston P;
 XX WPI; 1997-154262/14.
 DR N-PSDB; AAT70836.

PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
 PT inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of
 PT susceptibility to apoptotic disease.

XX Claim 27; Page 68-70; 21pp; English.

XX Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2
 CC (AA19581-86) are a new class of mammalian proteins that are inhibitors
 CC of apoptosis (IAP) and which are characterised by the presence of a ring
 CC zinc finger domain (see also AA19587) and at least one BIR (baculovirus
 CC IAP repeat) domain (see also AA19588). The XIAP amino acid sequence was
 CC deduced from the xiap gene (AAT70836) isolated from a human foetal brain
 CC cDNA library. IAP polypeptides can be expressed in host cells (in vitro
 CC or in vivo) and used in methods for treating diseases and disorders
 CC involving apoptosis, esp. in a human diagnosed as HIV-positive or as
 CC having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or
 CC an ischaemic injury, selected from myocardial infarction, stroke,
 CC reperfusion injury, or a toxin-induced liver disease

XX Sequence 497 AA;

Query Match 100.0%; Score 389; DB 2; Length 497;
 Best Local Similarity 100.0%; Pred. No. 1.3e-38;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPEQHAQWY 60
 DB 265 YEARIFTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPEQHAQWY 324
 QY 61 PGCKYL 66
 DB 325 PGCKYL 330

RESULT 5
 AA69294
 XX ID AA69294 standard; protein; 497 AA.
 AC AA69294;

XX
 DT 13-NOV-1998 (first entry)
 DE Human XIAP protein.

XX Inhibitor of apoptosis protein; apoptosis enhancer; NAP polypeptide;
 KW proliferative disease; IAP; therapy; cancer; human; XIAP protein.
 XX
 OS Homo sapiens.

XX WO9835693-A2.
 XX 20-AUG-1998.
 XX 13-FEB-1998; 98WO-IB000781.
 PF 13-FEB-1997; 97US-00800929.
 PR (UYOT-) UNIV OTTAWA.
 XX
 XX Korneluk R, Mackenzie AE, Liston P, Baird S, Tsang B, Pratt C;

XX WPI; 1998-467164/40.
 DR N-PSDB; AAV55038.

XX Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
 PT or NAI polypeptide - also methods for prognosis based on presence of IAP
 PT and NAI, specifically applied to cancers involving p53 mutations.

XX Disclosure; Fig 1; 147pp; English.

XX This sequence is the human XIAP protein, which is a inhibitor of
 CC apoptosis protein (IAP), and can be used in the method of the invention.
 CC The method is for enhancing apoptosis in cells from a mammal with

CC proliferative disease by treatment with a compound that inhibits
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory
 CC compounds are used to treat proliferative diseases, specially cancers of
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
 CC liver nasopharynx, thyroid, central nervous system, prostate, colon,
 CC rectum, cervix or endometrium, particularly to increase their sensitivity
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
 CC detected in many cancers and are associated with poor prognosis,
 CC resistance to chemotherapeutic agents and mutations in p53 (it is
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
 CC genes). Transgenic animals are used for testing the effects of antisense
 CC oligonucleotides and for screening for the inhibitors
 XX Sequence 497 AA;

Query Match 100.0%; Score 389; DB 2; Length 497;
 Best Local Similarity 100.0%; Pred. No. 1.3e-38;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEARIFTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWEQHAKEY 60
 Db 265 YEARIFTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWEQHAKEY 324
 QY 61 PGCKYL 66
 Db 325 PGCKYL 330

RESULT 6
 AAY59451
 ID AAY59451 standard; protein; 497 AA.
 XX
 AC AAY59451;
 XX
 DT 24-MAR-2000 (first entry)
 DE Human XIAP protein sequence.
 XX
 XX Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
 XX transforming growth factor-beta activated kinase 1; monocyte migration;
 XX TAK1 binding protein 1; extracellular matrix protein production;
 XX cell growth inhibitor; beta-amyloid protein deposition;
 XX immunosuppression; Transforming growth factor-beta.
 XX
 OS Homo sapiens.
 XX
 XX JP11326328-A.
 XX
 PD 26-NOV-1999.
 XX
 PP 13-MAY-1998; 98JP-00130378.
 XX
 PR 13-MAY-1998; 98JP-00130378.
 XX
 PA (MATSU) MATSUMOTO K.
 XX
 XX WPI; 2000-078337/07.
 DR N-PSDB; AAZ48862.
 XX

PT Screening a substance which inhibits combination of the X-linked
 PT inhibitor of apoptosis protein.
 XX

PS Claim 3; Page 28-30; 43pp; Japanese.

XX This sequence represents the human XIAP protein. The invention relates to
 CC a method for screening a substance inhibiting the formation of a complex
 CC between XIAP and TAB1, in which X-linked inhibitor of apoptosis protein
 CC (XIAP), transforming growth factor-beta activated kinase 1 (TAK1) binding
 CC protein 1 (TAB1) and a substance to be tested are contacted with each
 CC other and then the presence or formation of a complex between XIAP and
 CC TAB1 is detected. The substance can be used as a drug for extracellular
 CC matrix protein production enhancement, cell growth inhibition, monocyte
 CC migration, physiologically active substance induction, immunosuppression,

CC and beta-amyloid protein deposition. A substance inhibiting the formation
 CC of a complex between TAB1 and XIAP as well as between XIAP and TGF-beta
 CC (Transforming growth factor-beta) type I and/or type II receptor is
 CC useful as a drug
 XX
 SQ Sequence 497 AA;

Query Match 100.0%; Score 389; DB 3; Length 497;
 Best Local Similarity 100.0%; Pred. No. 1.3e-38;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEARIFTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWEQHAKEY 60
 Db 265 YEARIFTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWEQHAKEY 324

QY 61 PGCKYL 66
 Db 325 PGCKYL 330

RESULT 7
 AAY99985
 ID AAY99985 standard; protein; 497 AA.
 XX
 AC AAY99985;
 XX
 DT 07-NOV-2000 (first entry)
 DE Human X-linked inhibitor of apoptosis.
 XX
 XX X-linked inhibitor of apoptosis; XIAP; hILP; MHA; U45880; antisense;
 XX antiinflammatory; cytostatic; tumour.
 XX
 OS Homo sapiens.
 XX
 XX US6087173-A.
 XX
 PD 11-JUL-2000.
 XX
 PP 09-SEP-1999; 99US-00392580.
 XX
 PR 09-SEP-1999; 99US-00392580.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX
 XX Bennett CF, Cowsett LM, Ackermann EJ;
 XX
 XX WPI; 2000-498201/44.
 DR N-PSDB; AAA64901.
 XX

PT Antisense compound useful for research reagents, diagnostics, prophylaxis
 PT and for treating disorders associated with X-linked inhibitor of
 PT apoptosis, modulates expression of X-linked inhibitor of apoptosis.
 XX

Example 13; Col 43-48; 33pp; English.

XX The present invention relates to antisense oligonucleotides designed to
 CC inhibit expression of the human X-linked inhibitor of apoptosis (the
 CC present sequence). Modified phosphorothioate 2'-MOE oligonucleotides are
 CC more effective inhibitors than unmodified oligonucleotides. The
 CC oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis
 CC expression in cells and tissues in vitro. The oligonucleotides are also
 CC useful for treating animals or humans, prone to a disease associated with
 CC X-linked inhibitor of apoptosis. The oligonucleotides may also be used
 CC prophylactically to prevent infection, inflammation or tumour formation
 XX Sequence 497 AA;

Query Match 100.0%; Score 389; DB 3; Length 497;
 Best Local Similarity 100.0%; Pred. No. 1.3e-38;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEARIFTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWEQHAKEY 60

```
Db 265 YEARIFTGTWISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWEQHAHWY 324
QY 61 PGCKYL 66
Db 325 PGCKYL 330
RESULT 8
ABG65663
ID ABG65663 standard; protein; 497 AA.
XX
AC ABG65663;
XX
DT 26-AUG-2002 (first entry)
XX
DE Human inhibitor of apoptosis, XIAP.
XX
KW Human; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic;
KW cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer;
KW embryonic development; viral pathogenesis; autoimmune disorder;
KW neurodegenerative disease; multiple sclerosis; lupus erythematosus;
KW herpes virus infection; pox virus infection; adenovirus infection;
KW proliferative disease.
XX
OS Homo sapiens.
XX
PN WO200226968-A2.
XX
PD 04-APR-2002.
XX
PF 27-SEP-2001; 2001WO-CA001379.
XX
PR 28-SEP-2000; 2000US-00672717.
XX
PA (UYOT-) UNIV OTTAWA.
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX WPI; 2002-479562/51.
XX DR N-PSDB; ABK93869.
XX
PT Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
PT apoptosis in a cell, for treating cancer and other proliferative
PT diseases.
XX
PS Example 12; Fig 1; 135pp; English.
XX
CC The invention relates to an inhibitor of apoptosis (IAP) antisense
CC nucleic acid (I) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse or
CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC mammal diagnosed with a proliferative disease. The method is useful for
CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a human IAP
CC protein sequence
XX
SQ Sequence 497 AA;
Query Match 100.0%; Score 389; DB 5; Length 497;
Best Local Similarity 100.0%; Pred. NO. 1.3e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 1 YEARIFTGTWISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWEQHAHWY 60
Db 265 YEARIFTGTWISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWEQHAHWY 324
QY 61 PGCKYL 66
Db 325 PGCKYL 330
RESULT 9
ADB80961
ID ADB80961 standard; protein; 497 AA.
XX
AC ADB80961;
XX
DT 04-DEC-2003 (first entry)
XX
DE RING-SH complex related protein, SEQ ID NO 35.
XX
KW RING-SH 3; Gag protein; Gag late domain; PI3K; actin; myosin; Hsp60;
KW Hsp70; Hsp90; STAM1; STAM2A; STAM2B; VHS-UTM; GTPase; E2 enzyme; tsigl01;
KW cullin; RING-SH; clathrin; virucide; vaccine; antiviral; retrovirus;
KW rhadovirus; filovirus.
XX
OS Unidentified.
XX
PN WO2003033646-A2.
XX
PD 24-APR-2003.
XX
PF 31-JUL-2002; 2002WO-US024589.
XX
PR 31-JUL-2001; 2001US-0308958P.
XX
PR 09-NOV-2001; 2001US-0345846P.
XX
PA (PROT-) PROTEOLOGICS INC.
XX
PI Greener T, Moskowitz H, Reiss Y, Alroy I;
XX WPI; 2003-393509/37.
XX DR N-PSDB; ADB81002.
XX
PT New isolated protein complex comprising a RING-SH 3 polypeptide and
PT another polypeptide, useful for detecting cells infected with a virus,
PT and for treating viral disorders caused by retroviruses, thadoviruses,
PT or filoviruses.
XX
PS Disclosure; Fig 35; 176pp; English.
XX
CC The invention relates to a novel isolated protein complex comprising a
CC RING-SH 3 polypeptide and a polypeptide selected from a Gag protein, a
CC Gag late domain, PI3K, actin, myosin, Hsp60, Hsp70, Hsp90, STAM1, STAM2A,
CC STAM2B, VHS-UTM, a GTPase, an E2 enzyme, tsigl01, a cullin, RING-SH, and a
CC clathrin. The novel protein complex has virucide activity and can be used
CC to treat disorders as part of a vaccine. The protein complex and
CC composition are useful for detecting cells infected with a virus, for
CC identifying agents having antiviral activity, and for treating viral
CC disorders caused by retroviruses, rhadoviruses, or filoviruses. This
CC sequence is a protein comprising the RING-SH complex of the invention.
XX
SQ Sequence 497 AA;
Query Match 100.0%; Score 389; DB 7; Length 497;
Best Local Similarity 100.0%; Pred. NO. 1.3e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 YEARIFTGTWISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWEQHAHWY 60
Db 265 YEARIFTGTWISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWEQHAHWY 324
QY 61 PGCKYL 66
```



```
Query Match          94.6%; Score 368; DB 2; Length 496;
Best Local Similarity 95.5%; Pred. No. 4.7e-36;
Matches 63; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YEARIFTGTWTSYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPEQHAQWY 60
Db 264 YEARIVTFGTWTSYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPEQHAQWY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 12
ID AAW19584 standard; protein; 496 AA.
XX AAW19584;
XX DT 02-SEP-1997 (first entry)
XX DE Mouse apoptosis inhibitor M-XIAP.
XX KW Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; M-XIAP;
XX KW HIV; AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia;
XX KW myocardial infarction; stroke; reperfusion injury;
XX KW toxin-induced liver disease; gene therapy; diagnosis.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT Domain 26..93
XX FT /label= BIR-1
XX FT Domain 163..230
XX FT /label= BIR-2
XX FT Domain 264..329
XX FT /label= BIR-3
XX FT Domain 438..483
XX FT /label= Ring_zinc_finger
XX PN W09706255-A2.
XX PD 20-FEB-1997.
XX PF 05-AUG-1996; 96WO-IB001022.
XX PR 04-AUG-1995; 95US-00511485.
XX PR 22-DEC-1995; 95US-00576956.
XX PA (UYOT-) UNIV OTTAWA.
XX PI Korneluk RG, Mackenzie AE, Baird S, Liston P;
XX DR WPI; 1997-154262/14.
XX DR N-PSDB; AAT70839.
XX PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
XX PT inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of
XX PT susceptibility to apoptotic disease.
XX PS Claim 27; Page 79-80; 219pp; English.
XX CC Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2
XX CC (AAW19581-86) are a new class of mammalian proteins that are inhibitors
XX CC of apoptosis (IAP) and which are characterised by the presence of a ring
XX CC zinc finger domain (see also AAW19587) and at least one BIR (baculovirus
XX CC IAP repeated) domain (see also AAW19588). The M-XIAP amino acid sequence
XX CC was deduced from the m-xiap gene (AAT70839) isolated from a mouse embryo
XX CC cDNA library. The IAP polypeptides can be expressed in host cells (in
XX CC vitro or in vivo) and used in methods for treating diseases and disorders
XX CC involving apoptosis, esp. in a human diagnosed as HIV-positive or as
XX CC having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or
XX CC an ischaemic injury, selected from myocardial infarction, stroke,
```

```
CC reperfusion injury, or a toxin-induced liver disease
XX SQ Sequence 496 AA;

Query Match          94.1%; Score 366; DB 2; Length 496;
Best Local Similarity 95.5%; Pred. No. 8.2e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFTGTWTSYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPEQHAQWY 60
Db 264 YEARIVTFGTWTSYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPEQHAQWY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 13
AAW69297
ID AAW69297 standard; protein; 496 AA.
XX AAW69297;
XX DT 13-NOV-1998 (first entry)
XX DE Murine XIAP protein.
XX KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
XX KW proliferative disease; IAP; therapy; cancer; mouse; XIAP protein.
XX OS Mus sp.
XX PN W09835693-A2.
XX PD 20-AUG-1998.
XX PF 13-FEB-1998; 98WO-IB000781.
XX PR 13-FEB-1997; 97US-00800929.
XX PA (UYOT-) UNIV OTTAWA.
XX PI Korneluk R, Mackenzie AE, Liston P, Baird S, Tsang B, Pratt C;
XX DR WPI; 1998-467164/40.
XX DR N-PSDB; AAV55041.
XX PT Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
XX PT or NAIP polypeptide - also methods for prognosis based on presence of IAP
XX PT and NAIP, specifically applied to cancers involving p53 mutations.
XX PS Disclosure; Fig 4; 147pp; English.
XX CC This sequence is the murine XIAP protein, which is an inhibitor of
XX CC apoptosis protein (IAP), and can be used in the method of the invention.
XX CC The method is for enhancing apoptosis in cells from a mammal with
XX CC proliferative disease by treatment with a compound that inhibits
XX CC biological activity of an IAP or NAIP polypeptide. The inhibitory
XX CC compounds are used to treat proliferative diseases, specially cancers of
XX CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
XX CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,
XX CC rectum, cervix or endometrium, particularly to increase their sensitivity
XX CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
XX CC detected in many cancers and are associated with poor prognosis,
XX CC resistance to chemotherapeutic agents and mutations in p53 (it is
XX CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
XX CC genes). Transgenic animals are used for testing the effects of antisense
XX CC oligonucleotides and for screening for the inhibitors
XX SQ Sequence 496 AA;

Query Match          94.1%; Score 366; DB 2; Length 496;
Best Local Similarity 95.5%; Pred. No. 8.2e-36;
```


Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARIFTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPMQHAQWY 60
Db 264 YEARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPMQHAQWY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329
RESULT 14
ABG65666
ID ABG65666 standard; protein; 496 AA.
XX
AC ABG65666;
XX
DT 26-AUG-2002 (first entry)
XX
DE Mouse inhibitor of apoptosis, XIAP.
XX
KW Mouse; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic;
KW cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer;
KW embryonic development; viral pathogenesis; autoimmune disorder;
KW neurodegenerative disease; multiple sclerosis; lupus erythematosus;
KW herpes virus infection; pox virus infection; adenovirus infection;
KW proliferative disease.
XX
OS Mus sp.
XX
PN WO200226968-A2.
XX
PD 04-APR-2002.
XX
PF 27-SEP-2001; 2001WO-CA001379.
XX
PR 28-SEP-2000; 2000US-00672717.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI (AEGE-) AEGERA THERAPEUTICS INC.
XX
PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX
DR WPI; 2002-479562/51.
DR N-PSDB; ABK93872.
XX
PT Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
PT apoptosis in a cell, for treating cancer and other proliferative
PT diseases.
XX
PS Example 12; Fig 4; 135pp; English.
XX
CC The invention relates to an inhibitor of apoptosis (IAP) antisense
CC nucleic acid (I) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse or
CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC mammal diagnosed with a proliferative disease. The method is useful for
CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a mouse IAP
CC protein sequence
XX
SQ Sequence 496 AA;

Query Match 94.1%; Score 366; DB 5; Length 496;
Best Local Similarity 95.5%; Pred. No. 8.2e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARIFTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPMQHAQWY 60
Db 264 YEARIIVTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPMQHAQWY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329
RESULT 15
ADB61828
ID ADB61828 standard; protein; 66 AA.
XX
AC ADB61828;
XX
DT 04-DEC-2003 (first entry)
XX
DE Mouse inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
XX
KW baculovirus inhibitor of apoptosis repeat domain; BIR domain;
KW apoptosis pathway; embryonic development; viral pathogenesis; cancer;
KW autoimmune disorder; neurodegenerative disease; apoptotic response;
KW systemic lupus erythematosus; multiple sclerosis; viral infection;
KW herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
KW HIAP1; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
KW caspase-9; cytostatic; neoplasm; leukaemia; colon carcinoma;
KW cervical cancer; uterine cancer; testicular cancer;
KW small cell lung carcinoma; uterine cancer; renal cell carcinoma;
KW Wilm's tumour; BIR 3 domain; mouse; murine.
XX
OS Mus sp.
XX
PN WO2003040172-A2.
XX
PD 15-MAY-2003.
XX
PF 12-NOV-2002; 2002WO-CA001738.
XX
PR 09-NOV-2001; 2001US-0332300P.
PR 08-APR-2002; 2002US-0370934P.
XX
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
PI Boudreault A, Korneluk RG, La Casse E, Liston P;
XX
DR WPI; 2003-513532/48.
XX
PT Polypeptide capable of forming a complex with a polypeptide comprising a
PT baculovirus inhibitor of apoptosis repeat domain useful for treating
XX cancer and other neoplasms.
XX
PS Disclosure; Fig 1B; 53pp; English.
XX
CC This invention relates to a substantially pure polypeptide having a
CC length of less than 100 amino acids and capable of forming a complex with
CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
CC (BIR) domain. The apoptosis pathway is known to play a critical role in
CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
CC and neurodegenerative diseases. The failure of the apoptotic response has
CC been implicated in the development of cancer, autoimmune disorders (for
CC example systemic lupus erythematosus and multiple sclerosis) and viral
CC infections (including herpes virus, poxvirus and adenovirus. The
CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
CC (CIAP2) and HIAP2 (CIAP1) all possess three BIR domains and carboxy
CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
CC -9 which are proteases involved in the initiation of apoptosis. Compounds
CC which inhibit the activity of IAPs may therefore have cytostatic activity
CC through the enhancement of apoptosis. The polypeptides of the invention

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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:50:39 ; Search time 16.5 Seconds
(without alignments)
206.504 Million cell updates/sec

Title: US-09-654-743-25
Perfect score: 389
Sequence: 1 YEARIFTGTWYSVKNKEQL.....KPSDEPWEQAKWYPGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/2/iaa/PCUS COMB.pcp.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	389	100.0	66	2	US-08-511-485-25
2	389	100.0	66	4	US-09-201-936-25
3	389	100.0	66	4	US-09-011-356-25
4	389	100.0	236	4	US-09-239-867-4
5	389	100.0	497	2	US-08-511-485-4
6	389	100.0	497	3	US-09-212-971-4
7	389	100.0	497	3	US-08-800-929A-4
8	389	100.0	497	4	US-09-617-053A-4
9	389	100.0	497	4	US-08-657-759-2
10	389	100.0	497	4	US-09-201-936-4
11	389	100.0	497	4	US-09-011-356-4
12	389	100.0	497	4	US-09-672-717-219
13	366	94.1	66	2	US-08-511-485-24
14	366	94.1	66	4	US-09-201-936-24
15	366	94.1	66	4	US-09-011-356-24
16	366	94.1	496	2	US-08-511-485-10
17	366	94.1	496	3	US-09-212-971-10
18	366	94.1	496	3	US-08-800-929A-10
19	366	94.1	496	4	US-09-617-053A-10
20	366	94.1	496	4	US-09-201-936-10
21	366	94.1	496	4	US-09-011-356-10
22	366	94.1	496	4	US-09-672-717-225
23	347	89.2	236	3	US-09-121-979-4
24	347	89.2	236	4	US-09-332-319-4
25	347	89.2	236	4	US-09-239-867-2
26	295	75.8	53	4	US-08-657-759-19
27	249	64.0	50	3	US-08-975-080-28

28	249	64.0	50	3	US-08-975-080-29	Sequence 29, Appl
29	249	64.0	50	3	US-08-975-080-32	Sequence 32, Appl
30	211	54.2	68	2	US-08-511-485-26	Sequence 26, Appl
31	211	54.2	68	4	US-09-201-936-26	Sequence 26, Appl
32	211	54.2	68	4	US-09-011-356-26	Sequence 26, Appl
33	211	54.2	604	2	US-08-511-485-6	Sequence 6, Appl
34	211	54.2	604	3	US-09-212-971-6	Sequence 6, Appl
35	211	54.2	604	3	US-08-800-929A-6	Sequence 6, Appl
36	211	54.2	604	3	US-08-569-749-4	Sequence 4, Appl
37	211	54.2	604	4	US-09-617-053A-6	Sequence 6, Appl
38	211	54.2	604	4	US-09-201-936-6	Sequence 6, Appl
39	211	54.2	604	4	US-09-011-356-6	Sequence 6, Appl
40	211	54.2	604	4	US-09-672-717-221	Sequence 221, App
41	211	54.2	604	5	PCT-US96-12860-4	Sequence 4, Appl
42	205	52.7	68	2	US-08-511-485-28	Sequence 28, Appl
43	205	52.7	68	4	US-09-201-936-28	Sequence 28, Appl
44	205	52.7	68	4	US-09-011-356-28	Sequence 28, Appl
45	205	52.7	268	3	US-08-836-134-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-511-485-25
; Sequence 25, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
US-08-511-485-25

Query Match 100.0%; Score 389; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.7e-44;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWYSVKNKEQLARAGFYALGEGDKVCFHCGGLTDWKPSEDWEQAKWY 60
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Db 1 YEARIFTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 2
US-09-201-936-25
; Sequence 25, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201.936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011.356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576.956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511.485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-25

Query Match 100.0%; Score 389; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.7e-44;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 60
Db 1 YEARIFTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 3
US-09-011-356-25
; Sequence 25, Application US/09011356A
; Patent No. 656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011.356A
; EARLIER FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576.956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511.485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
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; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-011-356-25

Query Match 100.0%; Score 389; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.7e-44;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 60
Db 1 YEARIFTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 4
US-09-239-867-4
; Sequence 4, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239.867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073.001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-239-867-4

Query Match 100.0%; Score 389; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 8.2e-44;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 60
Db 4 YEARIFTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 63
QY 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 5
US-08-511-485-4
; Sequence 4, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-4

Query Match 100.0%; Score 389; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 2e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEARIFTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPEQHAQWY 60
Db 265 YEARIFTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPEQHAQWY 324
QY 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 6

US-09-212-971-4
Sequence 4, Application US/09212971B
Patent No. 6107041
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Teang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-09-212-971-4

Query Match 100.0%; Score 389; DB 3; Length 497;
Best Local Similarity 100.0%; Pred. No. 2e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEARIFTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPEQHAQWY 60
Db 265 YEARIFTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPEQHAQWY 324
QY 61 PGCKYL 66
Db 325 PGCKYL 330

Db 265 YEARIFTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPEQHAQWY 324
QY 61 PGCKYL 66
Db 325 PGCKYL 330
RESULT 7
US-08-800-929A-4
Sequence 4, Application US/08800929A
Patent No. 6133437
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Teang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERA
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-800-929A-4

Query Match 100.0%; Score 389; DB 3; Length 497;
Best Local Similarity 100.0%; Pred. No. 2e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEARIFTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPEQHAQWY 60
Db 265 YEARIFTGTWISYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPEQHAQWY 324
QY 61 PGCKYL 66
Db 325 PGCKYL 330

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RESULT 8
US-09-617-053A-4
; Sequence 4, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Teang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-617-053A-4
Query Match 100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEARIPTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAHWY 60
DB 265 YEARIPTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAHWY 324
QY 61 PGCKYL 66
DB 325 PGCKYL 330
;
RESULT 9
US-08-657-759-2
; Sequence 2, Application US/08657759
; Patent No. 6511828
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Dickett, Colin S.
; TITLE OF INVENTION: HUMAN AND DROSOPHILA INHIBITORS
; TITLE OF INVENTION: OF APOPTOSIS PROTEINS (IAPS)
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,759
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 497 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-657-759-2
Query Match 100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEARIPTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAHWY 60
DB 265 YEARIPTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAHWY 324
QY 61 PGCKYL 66
DB 325 PGCKYL 330
;
RESULT 10
US-09-201-936-4
; Sequence 4, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-4
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Best Local Similarity 100.0%; Pred. No. 2e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 PGCKYL 66
DB 325 PGCKYL 330
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RESULT 11
US-09-011-356-4
; Sequence 4, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
```

; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-011-356-4

Query Match 100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWTVSYNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWEQHAHWY 60
DB 265 YEARIFTGTWTVSYNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWEQHAHWY 324
QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 12

US-09-672-717-219
; Sequence 219, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean

; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; FILE REFERENCE: 07891/025001
; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 219
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-672-717-219

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DB 265 YEARIFTGTWTVSYNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWEQHAHWY 324
QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 13

US-08-511-485-24
; Sequence 24, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
US-08-511-485-24

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Best Local Similarity 95.5%; Pred. No. 2e-41; 2; Indels 0; Gaps 0;
Matches 63; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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DB 1 YEARIFTGTWTVSYNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWEQHAHWY 60
QY 61 PGCKYL 66
DB 61 PGCKYL 66

RESULT 14

US-09-201-936-24
; Sequence 24, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.

; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485

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; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-24

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Best Local Similarity 95.5%; Pred. No. 2e-41;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 61 PGCKYL 66
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Db 61 PGCKYL 66
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RESULT 15
US-09-011-356-24
; Sequence 24, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-011-356-24

Query Match          94.1%; Score 366; DB 4; Length 66;
Best Local Similarity 95.5%; Pred. No. 2e-41;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Search completed: March 10, 2004, 13:55:49
Job time : 16.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2004, 13:52:35 ; Search time 29 Seconds
(without alignments)
480.556 Million cell updates/sec

Title: US-09-654-743-25

Perfect score: 389

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Searched: 809742 seqs, 211153259 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	389	100.0	66	9 US-09-201-936-25	Sequence 25, Appl
2	389	100.0	107	9 US-09-965-967-20	Sequence 20, Appl
3	389	100.0	278	9 US-09-964-899-39	Sequence 39, Appl
4	389	100.0	497	9 US-09-974-592-4	Sequence 4, Appl
5	389	100.0	497	9 US-09-201-936-4	Sequence 24, Appl
6	366	94.1	66	9 US-09-201-936-24	Sequence 10, Appl
7	366	94.1	496	9 US-09-974-592-10	Sequence 10, Appl
8	366	94.1	496	9 US-09-201-936-10	Sequence 28, Appl
9	249	64.0	50	14 US-10-138-618-28	Sequence 29, Appl
10	249	64.0	50	14 US-10-138-618-29	Sequence 32, Appl
11	249	64.0	50	14 US-10-138-618-32	Sequence 26, Appl
12	211	54.2	68	9 US-09-201-936-26	Sequence 6, Appl
13	211	54.2	604	9 US-09-974-592-6	Sequence 6, Appl
14	211	54.2	604	9 US-09-201-936-6	Sequence 4, Appl
15	211	54.2	604	14 US-10-232-286-4	

16	211	54.2	604	14	US-10-141-618-6	Sequence 6, Appl
17	211	54.2	1140	14	US-10-353-461-8	Sequence 8, Appl
18	205	52.7	68	9	US-09-201-936-28	Sequence 28, Appl
19	205	52.7	68	14	US-10-041-859-18	Sequence 18, Appl
20	205	52.7	172	14	US-10-041-859-12	Sequence 12, Appl
21	205	52.7	268	14	US-10-323-643-10	Sequence 10, Appl
22	203	52.2	600	9	US-09-974-592-12	Sequence 12, Appl
23	199	51.2	68	14	US-10-041-859-14	Sequence 14, Appl
24	199	51.2	172	14	US-10-041-859-8	Sequence 8, Appl
25	199	51.2	346	14	US-10-041-859-2	Sequence 2, Appl
26	198	50.9	68	9	US-09-201-936-27	Sequence 27, Appl
27	198	50.9	618	9	US-08-974-592-8	Sequence 8, Appl
28	198	50.9	618	9	US-09-201-936-8	Sequence 8, Appl
29	197	50.6	438	8	US-08-464-588-2	Sequence 2, Appl
30	197	50.6	438	14	US-10-323-643-2	Sequence 2, Appl
31	197	50.6	602	9	US-09-201-936-40	Sequence 40, Appl
32	197	50.6	612	9	US-09-974-592-14	Sequence 14, Appl
33	197	50.6	612	14	US-10-232-286-14	Sequence 14, Appl
34	197	50.6	618	14	US-10-153-668-338	Sequence 338, Appl
35	197	50.6	618	14	US-10-207-655-200	Sequence 200, Appl
36	197	50.6	618	14	US-10-232-286-2	Sequence 2, Appl
37	194	49.9	68	14	US-10-041-859-19	Sequence 19, Appl
38	194	49.9	109	9	US-09-965-967-30	Sequence 30, Appl
39	194	49.9	172	14	US-10-041-859-13	Sequence 13, Appl
40	193	49.6	68	14	US-10-041-859-16	Sequence 16, Appl
41	193	49.6	172	14	US-10-041-859-10	Sequence 10, Appl
42	192	49.4	68	14	US-10-041-859-15	Sequence 15, Appl
43	192	49.4	172	14	US-10-041-859-9	Sequence 9, Appl
44	191	49.1	591	9	US-09-201-936-42	Sequence 42, Appl
45	190	48.8	68	9	US-09-201-936-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-09-201-936-25
; Sequence 25, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-25

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Best Local Similarity 100.0%; Pred. No. 1.5e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 YEARIPTGTWYVKNKEQLARAGFYALGSGDKVKCFCCGGTDMKPSDEPWEQRAK 60

QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 2

US-09-965-967-20
; Sequence 20, Application US/09965967
; Patent No. US20020177557A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yigong
; TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
; FILE REFERENCE: PU-0031 (01-1739-1)
; CURRENT APPLICATION NUMBER: US/09/965,967
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 607236, 574
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 607256, 830
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-967-20

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Best Local Similarity 100.0%; Pred. No. 2,6e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 15 YEARIPTGTWTVSYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWEQAKWY 74
QY 61 PGCKYL 66
Db 75 PGCKYL 80

RESULT 3

US-09-964-899-39
; Sequence 39, Application US/09964899
; Patent No. US20020174446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-964-899-39

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Best Local Similarity 100.0%; Pred. No. 7.1e-39;
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QY 61 PGCKYL 66

Db 106 PGCKYL 111

RESULT 4

US-09-974-592-4
; Sequence 4, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Teang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-592-4

Query Match 100.0%; Score 389; DB 9; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.3e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 265 YEARIPTGTWTVSYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWEQAKWY 324

QY 61 PGCKYL 66

Db 325 PGCKYL 330

RESULT 5

US-09-201-936-4
; Sequence 4, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens


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; Publication No. US20030100525A1
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; CELLULAR APOPTOSIS, AND ITS MODULATION
;
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,435
; FILING DATE: 20-NOV-1996
; PRIORITY APPLICATION NUMBER: US/10/138,618
; FILING DATE: 06-May-2002
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/975,080
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: US 60/031,435
; FILING DATE: 20-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
;
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
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;
; Query Match 64.0%; Score 249; DB 14; Length 50;
; Best Local Similarity 100.0%; Pred. No. 9.3e-23;
; Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 27 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWYPGCKYL 66
; DB 1 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWYPGCKYL 40
;
; RESULT 11
; US-10-138-618-32
; Sequence 32, Application US/10138618
; Publication No. US20030100525A1
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; CELLULAR APOPTOSIS, AND ITS MODULATION
;
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/138,618
; FILING DATE: 06-May-2002
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/975,080
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: US 60/031,435
; FILING DATE: 20-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
;
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
; US-10-138-618-28
;
; Query Match 64.0%; Score 249; DB 14; Length 50;
; Best Local Similarity 100.0%; Pred. No. 9.3e-23;
; Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 27 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWYPGCKYL 66
; DB 1 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWYPGCKYL 40
;
; RESULT 10
; US-10-138-618-29
; Sequence 29, Application US/10138618
; Publication No. US20030100525A1
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; CELLULAR APOPTOSIS, AND ITS MODULATION
;
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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;
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-138-618-32

Query Match          64.0%; Score 249; DB 14; Length 50;
Best Local Similarity 100.0%; Pred. No. 9.3e-23; Indels 0; Gaps 0;
Matches 40; Conservative 0; Mismatches 0;

QY 27 ALGEGDKVCFKFCGGGLTDWKPSDDPWEQHAKWYPGCKYL 66
   |||||
Db 1 ALGEGDKVCFKFCGGGLTDWKPSDDPWEQHAKWYPGCKYL 40

RESULT 12
US-09-201-936-26
; Sequence 26, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-26

Query Match          54.2%; Score 211; DB 9; Length 68;
Best Local Similarity 57.4%; Pred. No. 5e-18;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIFFGTWIYS--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPWEQHAK 58
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 HAARFKTFNWPSSVLNPEQLASAGFYVGNDDVKFCFCDGRLCWESGDPPWYQHAK 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 59 WYPGCKYL 66
   |||:|
Db 61 WFPRCEYL 68
   |||:|

RESULT 13
US-09-974-592-6
; Sequence 6, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
```

Sequence 4, Application US/10232286
Publication No. US2003014379A1
GENERAL INFORMATION:
APPLICANT: Roedel, Mike
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBRACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/232,286
FILING DATE: 30-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-232-286-4
Query Match 54.2%; Score 211; DB 14; Length 604;
Best Local Similarity 57.4%; Pred.No.5.le-17;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;
QY 1 YEARTFTGTWYS--VNKEQLARAGFYALCEGGKVKCFHCGGGLTDWKPESEDPWEQHAK 58
Db 255 HAARFTTFNWPSSVYNPEQLASAGFYVGNSDVKCFCCDGLRCWESGDDPWQHAK 314
QY 59 WYPGCKYL 66
Db 315 WPPRCEYL 322

Search completed: March 10, 2004, 13:56:59
Job time : 29 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:49:29 ; Search time 13 Seconds
(without alignments)
488.357 Million cell updates/sec

Title: US-09-654-743-25

Perfect score: 389

Sequence: 1 YEAFIFGTWISVNKEQL.....KPSDEPWEQHAQWPGCKYL 66

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	389	100.0	497	2 S69544	apoptosis inhibito
2	211	54.2	604	2 S68449	apoptosis inhibito
3	209	53.7	358	2 JC5964	apoptosis inhibito
4	205	52.7	268	2 T10304	inhibitor of apopt
5	205	52.7	268	2 A53989	apoptosis-inhibiti
6	198	50.9	618	2 S68450	apoptosis inhibito
7	190	48.8	275	2 A45679	inhibitor-of-apopt
8	188	48.3	298	2 JC7568	kidney inhibitor o
9	177.5	45.6	1232	2 A54478	neuronal apoptosis
10	174.5	44.9	1447	2 T42628	neuronal apoptosis
11	162	41.6	496	2 S68452	apoptosis inhibito
12	162	41.6	497	2 S69545	apoptosis inhibito
13	144	37.0	208	2 T03183	probable apoptosis
14	139	35.7	150	2 T28409	ORF MSV248 probabl
15	125	32.1	275	2 T10310	apoptosis-inhibiti
16	115.5	29.7	4845	2 T31067	apoptosis-inhibiti
17	111	28.5	286	2 D36828	BIR repeat contain
18	109	28.0	292	2 T41772	orf13 protein - Au
19	101	26.0	155	2 T30489	apoptosis inhibito
20	100	25.7	155	2 T37471	apoptosis inhibito
21	97	24.9	308	2 T37474	apoptosis inhibito
22	87.5	22.5	329	2 T28403	ORF MSV242 probabl
23	87.5	22.5	997	2 T43523	cutl17 protein - fi
24	79.5	20.4	564	2 C42523	ASR protein - vac
25	79.5	20.4	564	2 J01792	SalF17R protein -
26	66	17.0	576	1 ACFFA2	nicotinic acetylch
27	65	16.7	249	2 H72858	apoptosis inhibito
28	65	16.7	444	2 T15907	hypothetical prote
29	65	16.7	1808	2 T15099	hypothetical prote

30	64.5	16.6	557	2	S12359	nicotinic acetylch
31	64.5	16.6	737	2	PQ0219	RNA-2 polypeptid
32	63.5	16.3	506	2	S13720	coat protein ata
33	63.5	16.3	607	2	T39823	hypothetical prote
34	63	16.2	234	2	T30427	probable apoptosis
35	62.5	16.1	324	2	S39502	vegetative storage
36	62.5	16.1	532	2	A32751	vegetative storage
37	62	15.9	249	2	T41814	IAP2 orf71 - Bomby
38	62	15.9	474	2	S28419	lamin B-3 - mouse
39	62	15.9	592	2	B48315	lamin B2 - mouse
40	61	15.7	511	2	T43634	nicotinic acetylch
41	61	15.7	534	2	T25720	hypothetical prote
42	61	15.7	776	2	T29064	hyaluronate lyase
43	60	15.4	204	2	H70609	probable dna-3-met
44	60	15.4	246	2	I50127	MHC class II histo
45	60	15.4	252	2	I50126	MHC class II histo

ALIGNMENTS

RESULT 1

S69544

apoptosis inhibitor IAP homolog - human

C:Species: Homo sapiens (man)

C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000

C:Accession: S69544; S68451

R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan,

EMBO J. 15, 2685-2694, 1996

A:Title: A conserved family of cellular genes related to the baculovirus iap gene an

A:Reference number: S69544; MUID:96256286; PMID:8654366

A:Accession: S69544

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-497 <DUC>

A:Cross-references: EMBL:U32974; NID:gl016687; PIDN:AAC50518.1; PID:gl016688

R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farah,

Nature 379, 349-353, 1996

A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of

A:Reference number: A58182; MUID:96149249; PMID:8552191

A:Accession: S68451

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-161, 'C', 163-422, 'Q', 424-497 <LIS>

A:Cross-references: EMBL:U45880; NID:gl184319; PIDN:AAC50373.1; PID:gl184320

C:Genetics:

A:Gene: ilp

C:Function:

A:Description: apoptotic suppressor

C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology

C:Keywords: apoptosis; zinc finger

F:446-490/Domain: RING finger homology <RRN>

Query Match 100.0%; Score 389; DB 2; Length 497;

Best Local Similarity 100.0%; Pred. No. 7.8e-37;

Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEAFIFGTWISVNKEQLARAGFVALGEGDKVKCFHCGGLTDWKPSDPWEQHAQWY 60

Db 265 YEAFIFGTWISVNKEQLARAGFVALGEGDKVKCFHCGGLTDWKPSDPWEQHAQWY 324

QY 61 PGCKYL 66

Db 325 PGCKYL 330

RESULT 2

S68449

apoptosis inhibitor hiap-1 - human

C:Species: Homo sapiens (man)

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000

C:Accession: S68449

R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farah,

C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F;217-261/Domain: RING finger homology <RRN>

Query Match 52.7%; Score 205; DB 2; Length 268;
Best Local Similarity 50.0%; Pred. No. 5.5e-16;
Matches 33; Conservative 13; Mismatches 18; Indels 2; Gaps 1;

QY 3 ARIFTFGWISVNVK--EQIARAGFYALGEGDKVKCFHCGGGGLTDMKPSDDPWEQIAKWY 60
DB 113 ALRLTFASWPRLGKQRPPEELAEAGFFVTGGGDKTRCFCCDGGGLKDWEPDDAPWQQHARWY 172
|||
QY 61 PGCKYL 66
DB 173 DRCEYV 178
|||

RESULT 5
AS3989
apoptosis-inhibiting protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis;
C:Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMMFV
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 15-Sep-2000
R:Accession: A53989
R:Birnbaum, M.J.; Clem, R.J.; Miller, L.K.
J. Virol. 68, 2521-2528, 1994
A:Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a i
A:Reference number: A53989; MUID:94187094; PMID:8139034
A:Accession: A53989
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-268 <BI>
A:Cross-references: GB:L22564; NID:G456111; PIDN:RAB02610.1; PID:G456114
A:Note: authors translated the codon TGG for residue 28 as Tyr, GAC for residue 50;
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F;217-261/Domain: RING finger homology <RRN>

Query Match 52.7%; Score 205; DB 2; Length 268;
Best Local Similarity 50.0%; Pred. No. 5.5e-16;
Matches 33; Conservative 13; Mismatches 18; Indels 2; Gaps 1;

QY 3 ARIFTFGWISVNVK--EQIARAGFYALGEGDKVKCFHCGGGGLTDMKPSDDPWEQIAKWY 60
DB 113 ALRLTFASWPRLGKQRPPEELAEAGFFVTGGGDKTRCFCCDGGGLKDWEPDDAPWQQHARWY 172
|||
QY 61 PGCKYL 66
DB 173 DRCEYV 178
|||

RESULT 6
S68450
apoptosis inhibitor hiap-2 - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C:Accession: S68450
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faral
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family o
A:Reference number: A58182; MUID:96149249; PMID:8552151
A:Accession: S68450
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-618 <BS>
A:Cross-references: EMBL:U45879; NID:g1184317; PIDN:AACS0372.1; PID:g1184318
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: RING finger homology
C:Keywords: apoptosis; zinc finger
F;567-611/Domain: RING finger homology <RNG>

Query Match 50.9%; Score 198; DB 2; Length 618;
Best Local Similarity 52.9%; Pred. No. 7.9e-15;
Matches 36; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

S68452
apoptosis inhibitor diap - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Nov-2000
C:Accession: S68452; S78528
R/Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, N.; Nature 379, 349-353, 1996
A>Title: Suppression of apoptosis in mammalian cells by Nalp and a related family of IAP
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68452
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-496 <LIS>
A:Cross-references: EMBL:U45881; NID:G1184313; PIDN:AAC46988.1; PID:G1184314
R:Baird, S.D.
submitted to the EMBL Data Library, January 1996
A:Reference number: S78528
A:Accession: S78528
A:Molecule type: mRNA
A:Residues: 1-36 'AT', 37, 'K', 39, 'L', 41-44, 'H', 46-58, 'Q', 60-412, 'A', 414-427, 'A', 429-496 <
A:Cross-references: EMBL:U45881; NID:G1184313; PIDN:AAC46988.1; PID:G1184314
C:Genetics:
A:Cross-references: FlyBase:FBgn0015247
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C:Keywords: apoptosis; zinc finger
F:445-489/Domain: RING finger homology <RNG>

Query Match 41.6%; Score 162; DB 2; Length 496;
Best Local Similarity 43.3%; Pred. No. 8.6e-11;
Matches 29; Conservative 12; Mismatches 24; Indels 2; Gaps 1;

QY 2 EARFTFTGWIYS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPEWQHAKW 59
Db 211 DARLRTFTDPSINIQPASAQAAGLYQYKIGDQVRCFHCNIGLSWQKEDPEWQHAKW 270

QY 60 YPGCKYL 66
Db 271 SPKQCPV 277

RESULT 12
S69545
apoptosis inhibitor IAP homolog - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69545
R:Duckert, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M.C.; EMBO J. 15, 2885-2894, 1996
A>Title: A conserved family of cellular genes related to the baculovirus iap gene and ex
A:Reference number: S69544; MUID:96256286; PMID:8654366
A:Accession: S69545
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DUC>
A:Cross-references: EMBL:U32373; NID:G1019116; PIDN:AAC47155.1; PID:G1019117
C:Genetics:
A:Gene: iip
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
F:446-490/Domain: RING finger homology <RRN>

Query Match 41.6%; Score 162; DB 2; Length 497;
Best Local Similarity 43.3%; Pred. No. 8.6e-11;
Matches 29; Conservative 12; Mismatches 24; Indels 2; Gaps 1;

QY 2 EARFTFTGWIYS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPEWQHAKW 59
Db 213 DARLRTFTDPSINIQPASAQAAGLYQYKIGDQVRCFHCNIGLSWQKEDPEWQHAKW 272

QY 60 YPGCKYL 66
Db 273 SPKQCPV 279

RESULT 13

T03183
probable apoptosis inhibitor - Chilo iridescent virus
C:Species: Chilo iridescent virus
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Sep-2000
C:Accession: T03183
R:Bahr, U.; Tidona, C.A.; Darai, G.
Virus Genes 15, 235-245, 1997
A>Title: The DNA sequence of Chilo iridescent virus between the genome coordinates (
A:Reference number: Z14834; MUID:98141693; PMID:9482589
A:Accession: T03183
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-208 <BAH>
A:Cross-references: EMBL:AF003534; NID:G2738385; PIDN:AAB94481.1; PID:G2738454
C:Superfamily: RING finger homology
F:159-202/Domain: RING finger homology <RRN>

Query Match 37.0%; Score 144; DB 2; Length 208;
Best Local Similarity 45.0%; Pred. No. 4.2e-09;
Matches 27; Conservative 14; Mismatches 17; Indels 2; Gaps 1;

QY 1 YEARTFTGWIYSV--NKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPEWQHAK 58
Db 37 YDERLNSFQWFIQLPSKEQLSRAGFYLNIGVQVCFYCDLKLKEWKRSDNPFEEHKK 96

RESULT 14

T28409
ORF MSV248 probable inhibitor of apoptosis protein (IAP) - Melanoplus sanguinipes ei
C:Species: Melanoplus sanguinipes entomopoxvirus
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T28409
R:Atencio, C.B.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A>Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A:Reference number: Z20484; MUID:99102612; PMID:9847359
A:Accession: T28409
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-150 <AFO>
A:Cross-references: EMBL:AF063866; NID:G4049647; PIDN:AAC97724.1; PID:G4049764
C:Genetics:
A:Note: MSV248

Query Match 35.7%; Score 139; DB 2; Length 150;
Best Local Similarity 34.8%; Pred. No. 1.2e-08;
Matches 24; Conservative 14; Mismatches 25; Indels 6; Gaps 2;

QY 2 EARFTFTGWI----IYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPEWQHA 57
Db 17 QSRINSYENWPISLFFKINR--LCEAGFFYTNIGDITVCNCGLKIKNWLNYNDPWEIHS 74

QY 58 KNPYGGCKYL 66
Db 75 KNSPNCNYI 83

RESULT 15

T10310
apoptosis-inhibiting protein 1 - Orgyia pseudotsugata nuclear polyhedrosis virus
C:Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000
C:Accession: T10310
R:Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virology 229, 381-399, 1997
A>Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhed
A:Reference number: Z17011; MUID:97271300; PMID:9126251
A:Accession: T10310
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:42:54 ; Search time 10.5 Seconds
(without alignments)
327.298 Million cell updates/sec

Title: US-09-654-743-25

Perfect score: 389

Sequence: 1 YEARIFFGWIYVNKEQL.....KPSDDWEQHAQWYPCCKYL 66

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	389	100.0	497	1 BIR4 HUMAN	P98170 homo sapien
2	377	96.9	496	1 BIR4 RAT	Q9r016 rattus norv
3	368	94.6	496	1 BIR4 MOUSE	Q60989 mus musculus
4	347	89.2	236	1 BIR8 HUMAN	Q66009 homo sapien
5	341	87.7	236	1 BIR8 PANTR	Q95m72 pan troglod
6	338	86.9	236	1 BIR8 GORGO	Q95m71 gorilla gor
7	211	54.2	604	1 BIR3 HUMAN	Q13489 homo sapien
8	209	53.7	358	1 PIAP PIG	Q62640 sus scrofa
9	205	52.7	268	1 IAP3 NPVOP	P41437 orgyia pseu
10	204	52.4	611	1 BIR3 CHICK	Q90660 gallus gall
11	203	52.2	600	1 BIR3 MOUSE	Q08863 mus musculus
12	197	50.6	612	1 BIR2 MOUSE	Q62210 mus musculus
13	197	50.6	618	1 BIR2 HUMAN	Q13490 homo sapien
14	194	49.9	438	1 IAP1 DROME	Q24306 drosophila
15	190	48.8	275	1 IAP GVCP	P41436 cydia pomon
16	188	48.3	298	1 BIR7 HUMAN	Q96ca5 homo sapien
17	178.5	45.9	1403	1 BIR7 MOUSE	Q9jib6 mus musculus
18	177.5	45.6	1402	1 BIR7 MOUSE	Q9jib3 mus musculus
19	177.5	45.6	1403	1 BIR1 HUMAN	Q13075 homo sapien
20	177.5	45.6	1403	1 BIR4 MOUSE	Q9qwk5 mus musculus
21	177.5	45.6	1403	1 BIR5 MOUSE	Q9r016 mus musculus
22	174.5	44.9	1447	1 BIRB MOUSE	Q9qk44 mus musculus
23	162	41.6	498	1 IAP2 DROME	Q24307 drosophila
24	144	37.0	208	1 ZEP TRVS	P47732 chilo iride
25	129.5	33.3	142	1 BIR5 RAT	Q9jhw7 rattus norv
26	125	32.1	275	1 IAP1 NPVOP	Q10396 orgyia pseu
27	121.5	31.2	140	1 BIR5 MOUSE	Q70201 mus musculus
28	118.5	30.5	142	1 BIR5 HUMAN	Q15392 homo sapien
29	115.5	29.7	4829	1 BIR6 HUMAN	Q9nr09 homo sapien
30	111	28.5	286	1 IAP1 NPVAC	P41435 autographa
31	87.5	22.5	997	1 BIR1 SCHPO	Q14064 schizosacch
32	78.5	20.4	564	1 VA55 VACCC	P21073 vaccinia vi
33	79.5	20.4	564	1 VA55 VACCC	P24768 vaccinia vi

ALIGNMENTS

RESULT 1

ID	BIR4 HUMAN	STANDARD;	PRT;	497 AA.
AC	P98170; Q9NQL4;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)			
DE	(IAP-like protein) (HILP)			
GN	BIRC4 OR API3 OR IAP3 OR XIAP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Fetal brain;			
RX	MEDLINE=96149249; PubMed=8552191;			
RA	Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,			
RA	Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;			
RT	"Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes."			
RL	Nature 379:349-353(1996).			
(2)				
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Fetal heart;			
RX	MEDLINE=96256286; PubMed=8654366;			
RA	Duckett C.S., Nava V.B., Gedrich R.W., Clem R.J., van Dongen J.L.,			
RA	Gillfillan M.C., Shiels H., Hardwick J.M., Thompson C.B.;			
RT	"A conserved family of cellular genes related to the baculovirus iap gene and encoding apoptosis inhibitors."			
RL	EMBO J. 15:2685-2694(1996).			
(3)				
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Uterus;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Toquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			

34	71.5	18.4	224	1	IAPL ASPB7	Q65138 african swi
35	70.5	18.1	224	1	IAPL ASFMI	O1452 african swi
36	66.5	17.1	224	1	IAPL ASFCH	O12407 african swi
37	66	17.0	576	1	ACH2 DROME	P17644 drosophila
38	65.5	16.8	238	1	IAPL ASFMI	O11453 african swi
39	65	16.7	249	1	IAP2 NPVAC	P41454 autographa
40	64.5	16.6	557	1	ACH1 SCHGR	P23414 schistocerc
41	63.5	16.3	506	1	POL2 ARMV	P24819 arabis mosa
42	63.5	16.3	607	1	PESC SCHPO	O60164 schizosacch
43	62.5	16.1	224	1	IAPL ASFMI	O11451 african swi
44	62.5	16.1	436	1	ACHX ONCVC	P54247 onchocerca
45	62.5	16.1	532	1	SPER STRPU	P16264 strongyloce

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP FUNCTION.
RX MEDLINE=97373959; PubMed=9230442;
RA Deveraux Q.L., Takahashi R., Salvesen G.S., Reed J.C.;
RT "X-linked IAP is a direct inhibitor of cell-death proteases."
RL Nature 388:300-304(1997).
RN [6]
RP MUTAGENESIS OF ASP-148; ASP-214; ASN-259; TRP-310 AND GLU-314.
RX MEDLINE=21634829; PubMed=11604410;
RA Verhagen A.M., Silke J., Ekert P.G., Pakusch M., Kaufmann H.,
RA Connolly L.M., Day C.L., Tikoo A., Burke K., Wrobel C., Moritz R.L.,
RA Simpson R.J., Vaux D.L.;
RT "HtrA2 promotes cell death through its serine protease activity and
RT its ability to antagonize inhibitor of apoptosis proteins."
RL J. Biol. Chem. 277:445-454(2002).
RN [7]
RP STRUCTURE BY NMR OF 241-356 IN COMPLEX WITH SMAC.
RX MEDLINE=21020961; PubMed=1140637;
RA Liu Z., Sun C., Olejniczak E.T., Meadows R.P., Betz S.P., Oost T.,
RA Herrmann J., Wu J.C., Fesik S.W.;
RT "Structural basis for binding of Smac/Diablo to the XIAP BIR3
RT domain."
RL Nature 408:1004-1008(2000).
CC -!- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRS25 are mediated by the second
CC and third BIR domains.
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
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CC -----
CC EMBL; U45880; AAC50373.1; -;
CC EMBL; U32974; AAC50518.1; -;
CC EMBL; AL121601; CAB95312.1; -;
CC EMBL; BC032729; AAH32729.1; -;
CC PIR; S69544; S69544.
CC PDB; 1G3F; 10-JAN-01.
CC PDB; 1C9Q; 09-AUG-00.
CC PDB; 1P9X; 11-JUL-01.
CC PDB; 1G73; 10-JAN-01.
CC PDB; 1I30; 26-SEP-01.
CC PDB; 1I40; 31-OCT-01.
CC PDB; 1I51; 23-FEB-02.
CC PDB; 1KVC; 16-JAN-02.
CC PDB; 1KVC; 16-JAN-02.
CC Genex; HGNC:592; BIRC4.
CC MIM; 300079; -;
CC GO; GO:0005829; Cytosol; TAS.
CC GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
CC GO; GO:0006916; P:anti-apoptosis; TAS.
CC InterPro; IPR001370; BIR.
CC InterPro; IPR001841; Znf_ring.
CC Pfam; PF00653; BIR; 3.
CC SMART; SM00238; BIR; 3.
CC SMART; SM00184; RING; 1.

DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0158; ZF_RING_1; FALSE NEG.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat; Thiol protease inhibitor;
KW 3D-structure.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 265 330 BIR 3.
FT ZN_FING 450 485 RING-TYPE.
FT MUTAGEN 214 214 D->S: DECREASED INTERACTION WITH PRS25.
FT MUTAGEN 314 314 E->S: DECREASED INTERACTION WITH SMAC AND
FT WITH PRS25.
FT CONFLICT 162 162 S -> C (IN REF. 1).
FT CONFLICT 423 423 Q -> P (IN REF. 2).
SQ SEQUENCE 497 AA; 56684 MW; 9D394CL6D45EB635 CRC64;
Query Match 100.0%; Score 389; DB 1; Length 497;
Best Local Similarity 100.0%; Pred. No. 7.9e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEARIETGWTIYSYNNKEQLARAGYALGEGDKVKCFHCGGLTDWKPSDPWEQAKWY 60
Db 265 YEARIETGWTIYSYNNKEQLARAGYALGEGDKVKCFHCGGLTDWKPSDPWEQAKWY 324
QY 61 PGCKYL 66
Db 325 PGCKYL 330
RESULT 2
BIR4 RAT STANDARD; PRT; 496 AA.
ID BIR4 RAT
AC Q9R016;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (RIAP3) (RIAP-3).
OS Rattus norvegicus (Rat).
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Saito N.;
RT "Rattus norvegicus X-linked inhibitor of apoptosis (riap3) mRNA."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
CC (By similarity).
CC -!- SUBUNIT: Interacts with SMAC and with PRS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRS25 are mediated by the second
CC and third BIR domains (By similarity).
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
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CC -----
CC EMBL; AB033366; BAA85304.1; -;
CC HSP; Q13490; IQBH.

```
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR SMART; SMO0238; BIR; 3.
DR SMART; SMO0184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 264 329 BIR 3.
FT ZN_FING 449 484 RING-TYPE.
SQ SEQUENCE 496 AA; 56072 MW; E250B3C77461A469 CRC64;

Query Match 96.9%; Score 377; DB 1; Length 496;
Best Local Similarity 95.5%; Pred. No. 2e-36; 1; Indels 0; Gaps 0;
Matches 63; Conservative 2; Mismatches 1;

QY 1 YEARIFTGTWYISVNVKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPEQHKWY 60
DB 264 YDARIVTGTWYISVNVKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPEQHKWY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 3
ID BIR4_MOUSE STANDARD; PRT; 496 AA.
AC Q60989; O08865;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (MIAP3) (MIAP-3).
GN BIR4 OR API3 OR XIAP OR AIPA OR MIAA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Farahani R., Lefebvre C., Korneluk R.G., Mackenzie A.E.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
CC (By similarity)
CC -! SUBUNIT: Interacts with SMAC and with PRS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -! DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRS25 are mediated by the second
CC and third BIR domains (By similarity).
CC -! SIMILARITY: Belongs to the IAP family.
CC -! SIMILARITY: Contains 3 BIR repeats.
CC -! SIMILARITY: Contains 1 RING-type zinc finger.
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CC or send an email to license@isb-sib.ch).
DR EMBL; U86842; AAC52594.1; -.
DR EMBL; U89990; AAB58376.1; -.
DR HSP; Q13490; IQBH.
DR MGD; MGI:107572; Birc4.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 3.
DR SMART; SMO0238; BIR; 3.
DR SMART; SMO0184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 264 329 BIR 3.
FT ZN_FING 449 484 RING-TYPE.
FT CONFLICT 208 208 E -> K (IN REF. 2).
FT CONFLICT 317 317 E -> D (IN REF. 2).
FT CONFLICT 322 322 W -> C (IN REF. 2).
FT CONFLICT 346 346 S -> P (IN REF. 2).
FT CONFLICT 360 360 S -> P (IN REF. 2).
FT CONFLICT 388 388 I -> L (IN REF. 2).
FT CONFLICT 449 449 C -> S (IN REF. 2).
FT CONFLICT 462 462 V -> F (IN REF. 2).
FT CONFLICT 468 468 V -> A (IN REF. 2).
FT CONFLICT 490 490 K -> N (IN REF. 2).
SQ SEQUENCE 496 AA; 56079 MW; EC5FAE0799F2CDD8 CRC64;

Query Match 94.6%; Score 368; DB 1; Length 496;
Best Local Similarity 95.5%; Pred. No. 2e-35;
Matches 63; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YEARIFTGTWYISVNVKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPEQHKWY 60
DB 264 YEARIFTGTWYISVNVKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPEQHKWY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 4
ID BIR8_HUMAN STANDARD; PRT; 236 AA.
AC Q96P09; Q96RW5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2) (Testis-specific
DE inhibitor of apoptosis).
GN BIRC8 OR ILP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=21481900; PubMed=11597143;
RA Lagace M., Xuan J.-f., Young S.S., McRoberts C., Maier J.,
RA Rajcan-Separovic E., Korneluk R.G.;
RT "Genomic organization of the X-linked inhibitor of apoptosis and
RT identification of a novel testis-specific transcript.";
RL Genomics 77:181-188 (2001).
RN [2]
```

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SEQUENCE FROM N.A.
RA MEDLINE=21286921; PubMed=11390657;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Refey S.B.,
RA Frattini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezzoni P., Fearnhead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family.";
RT Mol. Cell. Biol. 21:4292-4301(2001).
CC -!- FUNCTION: Protects against apoptosis mediated by BAX. (By
CC similarity).
CC -!- SUBUNIT: Binds to caspase-9.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- TISSUE SPECIFICITY: Testis specific in normal tissues.
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 1 BIR repeat.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC -----
EMBL: AF420440; AAL30369.1; -.
DR EMBL; AF164682; AAK81892.1; -.
DR Genew; HGNC:14878; BIRC8.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS00518; BIR_REPEAT_2; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger.
KW REPEAT
FT REPEAT 7 70 BIR.
FT ZN FING 189 224 RING-TYPE.
FT CONFLICT 196 196 Y -> H (IN REF. 2).
FT SEQUENCE 236 AA; 27115 MW; CB7F034B0DDFAD9D CRC64;
Query Match 89.2%; Score 347; DB 1; Length 236;
Best Local Similarity 84.8%; Pred. No. 2.9e-33; Indels 0; Gaps 0;
Matches 56; Conservative 6; Mismatches 4;
QY 1 YEARIFFGTWYISVNKEQLARAGFYALGEGDKVCFHCGGLTDWKPSPDPWEQHAQWY 60
Db 4 YEARIITFTWYISVNKEQLARAGFYALGEGDKVCFHCGGLTDWKPSPDPWEQHAQWY 63
QY 61 PGCKYL 66
Db 64 PGCKYL 69
RESULT 5
BIRS_PANTR STANDARD; PRT; 236 AA.
ID BIRS_PANTR
AC Q95M72;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2).
GN BIRC8 OR ILP2.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A. PubMed=11390657;
RX MEDLINE=21286921; PubMed=11390657;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Refey S.B.,

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RA Frattini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezzoni P., Fearnhead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family.";
RT Mol. Cell. Biol. 21:4292-4301(2001).
CC -!- FUNCTION: Protects against apoptosis mediated by BAX (By
CC similarity).
CC -!- SUBUNIT: Binds to caspase-9 (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 1 BIR repeat.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC -----
EMBL: AY030052; AAK49776.1; -.
DR EMBL; AY030052; AAK49776.1; -.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS00518; BIR_REPEAT_2; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger.
KW REPEAT
FT REPEAT 7 70 BIR.
FT ZN FING 189 224 RING-TYPE.
FT SEQUENCE 236 AA; 27136 MW; 64CCA3A251420EDE CRC64;
Query Match 87.7%; Score 341; DB 1; Length 236;
Best Local Similarity 83.3%; Pred. No. 1.4e-32;
Matches 55; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 1 YEARIFFGTWYISVNKEQLARAGFYALGEGDKVCFHCGGLTDWKPSPDPWEQHAQWY 60
Db 4 YEARIITFTWYISVNKEQLARAGFYALGEGDKVCFHCGGLTDWKPSPDPWEQHAQWY 63
QY 61 PGCKYL 66
Db 64 PGCKYL 69
RESULT 6
BIRS_GORGO STANDARD; PRT; 236 AA.
ID BIRS_GORGO
AC Q95W71;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2).
GN BIRC8 OR ILP2.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A. PubMed=11390657;
RX MEDLINE=21286921; PubMed=11390657;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Refey S.B.,
RA Frattini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezzoni P., Fearnhead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family.";
RT Mol. Cell. Biol. 21:4292-4301(2001).
CC -!- FUNCTION: Protects against apoptosis mediated by BAX (By

```

CC similarity).

CC -!- SUBUNIT: Binds to caspase-9 (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).

CC -!- SIMILARITY: Belongs to the IAP family.

CC -!- SIMILARITY: Contains 1 BIR repeat.

CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

CC -----

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CC -----

DR EMBL; AY030053; AAK49777.1; ..

DR InterPro; IPR001370; BIR.

DR InterPro; IPR001841; Znf_ring.

DR Pfam; PF00653; BIR; 1.

DR SMART; SM00238; BIR; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01282; BIR_REPEAT_1; FALSE_NEG.

DR PROSITE; PS0143; BIR_REPEAT_2; 1.

DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.

DR PROSITE; PS0089; ZF_RING_2; 1.

KW Apoptosis; Zinc-finger.

FT REPEAT 7 70

FT ZN FING 189 224 RING-TYPE.

FT ZN FING 236 AA; 27120 MW; C3A70E39E442E4C CRC64;

SQ SEQUENCE 236 AA; 27120 MW; C3A70E39E442E4C CRC64;

Query Match 86.9%; Score 338; DB 1; Length 236;

Best Local Similarity 81.8%; Pred. No. 3.2e-32;

Matches 54; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 YEARTFTFTWTSYVNKQLARAGFYALGEGDKVCFHCGGLTDWKPSPDPWEQIAKWY 60

DB 4 YEAWLITFTWTSYVNKQLARAGFYALGEGDKVCFHCGGLANWKPEDPWEQIAKWY 63

QY 61 PGCKYL 66

DB 64 PGCKYL 69

RESULT 7

BIR3_HUMAN STANDARD; PRT; 604 AA.

AC Q13489; Q16628; Q9HC27; Q9UP46;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Baculoviral IAP repeat-containing protein 3 (inhibitor of apoptosis

DE protein 1) (HIAP1) (HIAP-1) (C-IAP2) (TNFR2-TRAF signaling complex

DE protein 1) (IAP homolog C) (Apoptosis inhibitor 2) (API2).

GN BIRC3 OR API2 OR IAPI OR MIHC.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RX SEQUENCE FROM N.A.

RX MEDLINE=96128127; PubMed=8548910;

RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;

RT "The TNFR2-TRAF signaling complex contains two novel proteins related

RT to baculoviral inhibitor of apoptosis proteins.";

RL Cell 83:1243-1252 (1995).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=96149249; PubMed=8552191;

RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,

RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;

RT "Suppression of apoptosis in mammalian cells by NAIP and a related

RT family of IAP genes.";

RL Nature 379:349-353 (1996).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Fetal liver;

RX MEDLINE=96209843; PubMed=8643514;

RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;

RT "Cloning and expression of apoptosis inhibitory protein homologs that

RT function to inhibit apoptosis and/or bind tumor necrosis factor

RT receptor-associated factors.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978 (1996).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=9925096; PubMed=10233894;

RA Horrevorts A.J., Fontijn R.D., van Zonneveld A.J., de Vries C.J.,

RA ten Cate J.W., Pannekoek H.;

RT "Vascular endothelial genes that are responsive to tumor necrosis

RT factor-alpha in vitro are expressed in atherosclerotic lesions,

RT including inhibitor of apoptosis protein-1, stannin, and two novel

RT genes.";

RL Blood 93:3418-3431 (1999).

RN [5]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymph;

RX MEDLINE=22398257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [6]

RP SEQUENCE OF 362-441 FROM N.A.

RX MEDLINE=20519161; PubMed=11066071;

RA Baens M., Steyls A., Dierlamm J., De Wolf-Peeters C., Marynen P.;

RT "Structure of the MTR gene and molecular characterization of the

RT genomic breakpoint junctions in the t(11;18)(q21;q21) of marginal zone

RT B-cell lymphomas of MALT type.";

RL Genes Chromosomes Cancer 29:281-291 (2000).

CC -!- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS

CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO

CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR

CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).

CC -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions

CC inhibit apoptotic suppressor activity.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL LUNG, AND KIDNEY. IN

CC THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES,

CC INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.

CC -!- DISEASE: INVOLVED IN A t(11;18)(q21;q21) CHROMOSOMAL TRANSLOCATION

CC RECURRENT IN LOW-GRADE MALT LYMPHOMA (MUCOSA-ASSOCIATED LYMPHOID

CC TISSUE). THIS TRANSLOCATION IS FOUND IN APPROXIMATELY 50% OF

CC CYTOGENETICALLY ABNORMAL LOW-GRADE MALT LYMPHOMA AND INVOLVES

CC MALT1 AND BIRC3.

CC -!- SIMILARITY: Belongs to the IAP family.

CC -!- SIMILARITY: Contains 3 BIR repeats.

CC -!- SIMILARITY: Contains 1 CARD domain.

CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;

CC WWW="http://www.infobiogen.fr/services/chronocancer/BIRC3ID239.html".

GN IAP3 OR IAP
 OS Orygia pseudotsugata multicapsid polyhedrosis virus (OpMPV).
 CC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 CC Nucleopolyhedrovirus.
 OX NCBI_TaxID=164623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94187094; PubMed=8139034;
 RA Birnbaum M.J., Clem R.J., Miller L.K.;
 RT "An apoptosis-inhibiting gene from a nuclear polyhedrosis virus
 RL encoding a polypeptide with Cys/His sequence motifs.";
 J. Virol. 68:2521-2528(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97271300; PubMed=9126351;
 RA Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
 RA Rohrmann G.F.;
 RT "The sequence of the Orygia pseudotsugata multinucleocapsid nuclear
 RL polyhedrosis virus genome.";
 RL Virology 229:381-399(1997).
 CC -!- FUNCTION: ACTS BY BLOCKING CELLULAR APOPTOSIS RATHER THAN BY
 CC PREVENTING VIRAL STIMULATION OF APOPTOSIS.
 CC -!- SIMILARITY: Contains 2 BIR repeats.
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
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 CC -----
 DR EMBL; L22564; AAB02610.1; .
 DR EMBL; U75930; AAC59034.1; .
 DR PIR; A53989; A53989.
 DR HSSP; Q13490; IQBH.
 DR InterPro; IPR001370; BIR.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00653; BIR; 2.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00238; BIR; 2.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; 2.
 DR PROSITE; PS0143; BIR_REPEAT_2; 2.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS00089; ZF_RING_2; 1.
 KW Apoptosis; Zinc-finger; Repeat.
 FT REPEAT 18 84
 FT REPEAT 111 178
 FT ZN_FING 221 256
 FT SEQUENCE 269 AA; 30076 MW; D89175FDE85A708 CRC64;
 Query Match 52.7%; Score 205; DB 1; Length 268;
 Best Local Similarity 50.0%; Pred. No. 1.e-16;
 Matches 33; Conservative 13; Mismatches 18; Indels 2; Gaps 1;
 QY 3 ARIFTFGTWISVVK--EOLARAGFYALGEGDKVKCPHCGGLTDWKPSPDPWEQAKVY 60
 DB 113 ALRLTFAEWPRGLKORPELAENGFTYGGQDKTRCFCCDGLKDWEPDDAPWQOHARWY 172
 QY 61 PCKYKL 66
 DB 173 DRCEV 178
 RESULT 10
 BIR_CHK
 ID BIR_CHK STANDARD; PRT; 611 AA.
 AC Q90660; O57319;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Inhibitor of apoptosis protein (IAP) (Inhibitor of T cell apoptosis
 DE protein).
 GN ITA OR IAP1.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97101112; PubMed=8945639;
 RA Dieby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal J.W.;
 RT "ITA, a vertebrate homologue of IAP that is expressed in T
 RT lymphocytes.";
 RN DNA Cell Biol. 15:981-988(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White leghorn; TISSUE=Embryonic fibroblast;
 RX MEDLINE=98038801; PubMed=9372964;
 RA You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;
 RT "ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a
 RT mediator of the antiapoptotic activity of the v-Rel oncoprotein.";
 RL Mol. Cell. Biol. 17:7328-7341(1997).
 CC -!- FUNCTION: Apoptotic suppressor.
 CC -!- SUBCELLULAR LOCATION: Predominantly nuclear. Cytoplasmic
 CC according to Ref. 2.
 CC -!- TISSUE SPECIFICITY: Cells of the T lymphocyte lineage. Found in
 CC both cortical and medullary cells of the thymus. Expressed at
 CC relatively high levels also in spleen, bursa, intestine and lung
 CC and at very low levels in testis, brain and skeletal muscle.
 CC -!- INDUCTION: High levels are induced within 4-8 hours of T-cell
 CC activation in spleen and thymus.
 CC -!- DOMAIN: The ring finger is important for its antiapoptotic effect.
 CC -!- SIMILARITY: Belongs to the IAP family.
 CC -!- SIMILARITY: Contains 3 BIR repeats.
 CC -!- SIMILARITY: Contains 1 CARD domain.
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
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 CC -----
 DR EMBL; U27466; AAB48118.1; .
 DR EMBL; AF008592; AAB88044.1; .
 DR HSSP; Q13490; IQBH.
 DR InterPro; IPR001370; BIR.
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00653; BIR; 3.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00238; BIR; 3.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; 3.
 DR PROSITE; PS0143; BIR_REPEAT_2; 3.
 DR PROSITE; PS0209; CARD; 1.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS00089; ZF_RING_2; 1.
 KW Apoptosis; Zinc-finger; Repeat; Nuclear protein.
 FT REPEAT 30 97
 FT REPEAT 176 242
 FT REPEAT 262 329
 FT REPEAT 446 536
 FT DOMAIN 446 536
 FT ZN_FING 564 599
 FT CONFLICT 27 27
 FT CONFLICT 150 150
 FT CONFLICT 169 169

```
FT CONFLICT 183 193 S -> F (IN REF. 2).
FT CONFLICT 196 192 CLW -> FLU (IN REF. 2).
FT CONFLICT 196 196 V -> L (IN REF. 2).
FT CONFLICT 202 203 DD -> YY (IN REF. 2).
FT CONFLICT 213 214 VN -> FT (IN REF. 2).
FT CONFLICT 217 218 VK -> GQ (IN REF. 2).
FT CONFLICT 350 355 WNSST -> ELLS (IN REF. 2).
FT CONFLICT 359 359 K -> T (IN REF. 2).
FT CONFLICT 426 426 E -> D (IN REF. 2).
FT CONFLICT 492 492 T -> K (IN REF. 2).
FT CONFLICT 497 497 S -> L (IN REF. 2).
FT CONFLICT 524 524 F -> C (IN REF. 2).
SQ SEQUENCE 611 AA; 69009 MW; 53FC9136F34EBDDD CRC64;

Query Match 52.4%; Score 204; DB 1; Length 611;
Best Local Similarity 54.4%; Pred. No. 3.4e-16;
Matches 37; Conservative 8; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIPTFTGTW--IYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWEQHAH 58
Db 262 HEARVNTFINWPRIPVQPEQLADAGFYVYVGRNDDVKCFCDGGLRCWESGDDPWVEHAK 321

QY 59 WYPGCKYL 66
Db 322 WPRCEYL 329

RESULT 11
ID_BIR3_MOUSE STANDARD; PRT; 600 AA.
AC O08863;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis
DE protein 1) (MIAP1) (MIAP-1).
GN BIRC3 OR BIRC3 OR IAP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes."
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U88908; AAC53531.1; -
CC HSSP; Q13490; 1QBH.
CC MGD; MGI:1197007; Birc2.
CC InterPro; IPR001370; BIR.
```

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DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF0653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 27 94 BIR 1.
FT REPEAT 167 233 BIR 2.
FT REPEAT 253 320 BIR 3.
FT DOMAIN 436 525 CARD.
FT ZN_FING 553 588 RING-TYPE.
SQ SEQUENCE 600 AA; 67198 MW; AD7F73E6849317D1 CRC64;

Query Match 52.2%; Score 203; DB 1; Length 600;
Best Local Similarity 52.9%; Pred. No. 4.4e-16;
Matches 36; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIPTFTGTWYS--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWEQHAH 58
Db 253 HAARITFTSNPSSALVHSQELASAGFYTGHSDDVKCFCDGGLRCWESGDDPWVEHAK 312

QY 59 WYPGCKYL 66
Db 313 WPRCEYL 320

RESULT 12
ID_BIR2_MOUSE STANDARD; PRT; 612 AA.
AC Q62210; O08864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis
DE protein 2) (MIAP2) (MIAP-2).
GN BIRC2 OR BIRC3 OR IAP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE=96128127; PubMed=8548910;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins."
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes."
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: Expressed in heart, brain, spleen, lung,
CC liver, skeletal muscle, kidney and testis.
CC -1- SIMILARITY: Belongs to the IAP family.
```

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CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC -----
DR EMBL; L49433; AAC42078.1; .
DR EMBL; U88909; AAC53532.1; .
DR HSP; Q13490; LOBH.
DR MGD; MG1:1197009; Birc3.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 46 113 BIR 1.
FT REPEAT 177 243 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 447 537 CARD.
FT ZN FING 565 600 RING-TYPE.
FT CONFLICT 380 380 E -> K (IN REF. 2).
SQ SEQUENCE 612 AA; 69676 MW; E08969D93C6C610D CRC64;

Query Match 50.6%; Score 197; DB 1; Length 612;
Best Local Similarity 52.9%; Pred. No. 2.3e-15;
Matches 36; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARTPTFTWYS--VNKEQLARAGFYALGEGKVKCFCHGGLTKWKSDEPWEGHAK 58
Db 262 HSARLTFTLWPPVFPVQEQALASGFYVNDNDVKCFCDGGLRCWEPGDDPWIEHAK 321
QY 59 WYPGCKYL 66
Db 322 WFPRCFEL 329

RESULT 13
BIR2_HUMAN STANDARD; PRT; 618 AA.
AC Q13490; Q16516;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis
DE protein 2) (HIAP2) (HIAP-2) (C-IAP1) (TNFR2-TRAF signaling complex
DE protein 2) (IAP homolog B).
GN BIRC2 OR API1 OR IAP2 OR MIHB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=96128127; PubMed=8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins.";

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RL Cell 83:1243-1252 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96149249; PubMed=8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes.";
RL Nature 379:349-353 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978 (1996).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis, and Uterus;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madao A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP STRUCTURE BY NMR OF 266-363.
RX MEDLINE=99332054; PubMed=10404221;
RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;
RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP)
RT repeat.";
RL Nat. Struct. Biol. 6:648-651 (1999).
CC -!- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.
CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,
CC AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD
CC LEUKOCYTES.
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
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CC -----
DR EMBL; L49431; AAC41942.1; -.
DR EMBL; U45879; AAC50372.1; -.
DR EMBL; U37547; AAC50508.1; -.
DR EMBL; BC016174; AAH16174.1; -.
DR EMBL; SC028578; AAH28578.1; -.
DR FIR; S68450; S68450.
DR PDB; 1QBH; 20-OCT-99.
DR Genew; HGNC:590; BIRC2.
DR MIM; 601712; -.
DR GO; GO:0008189; P:apoptosis inhibitor activity; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; ZF-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat; 3D-structure.
FT REPEAT 46 113
FT REPEAT 184 250
FT REPEAT 269 326
FT REPEAT 453 543
FT DOMAIN
FT ZN_RING 571 606
FT CONFLICT 157 157 S -> P (IN REF. 2).
FT CONFLICT 308 308 C -> G (IN REF. 2).
FT CONFLICT 414 414 Q -> L (IN REF. 2).
FT CONFLICT 514 514 L -> W (IN REF. 2).
FT TURN 269 270
FT TURN 271 274
FT HELIX 271 293
FT TURN 294 294
FT TURN 296 297
FT TURN 301 304
FT STRAND 309 309
FT HELIX 322 325
FT TURN 326 328
FT STRAND 333 333
FT TURN 334 343
FT HELIX 344 351
FT TURN 353 354
SQ SEQUENCE 618 AA; 69899 MW; C1778D328063586D CRC64;

Query Match 50.6%; Score 197; DB 1; Length 618;
Best Local Similarity 52.9%; Pred. No. 2.3e-15;
Matches 36; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEALIFPGTWIYS--VNKQLARAGFYALGEGDKVKCFHCGGLTDMKPSDEDWEQHAQ 58
DB 269 HAARMRTFMYPPSSVPQPSQLASAGFYVGRNDYKCFCCDGLRCWESGDPPWEHAK 328
QY 59 WYPGCKYL 66
DB 329 WPRCEFL 336

RESULT 14
IAP1_DROME
ID IAP1_DROME STANDARD; PRT; 438 AA.
AC Q24306;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Apoptosis 1 inhibitor (inhibitor of apoptosis 1) (diap1) (Thread
protein).

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GN IAP1 OR TH.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=eye imaginal disk;
RX MEDLINE=96128128; PubMed=9548811;
RA Hay B.A., Wasserman D.A., Rubin G.M.;
RT "Drosophila homologs of baculovirus inhibitor of apoptosis proteins
function to block cell death.";
RL Cell 83:1253-1262(1995).
CC -!- FUNCTION: APOPTOTIC SUPPRESSOR. OVEREXPRESSION SUPPRESSES RPR AND
CC -!- H1D-DEPENDENT CELL DEATH IN THE EYE.
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 2 BIR repeats.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC -----
DR EMBL; L49440; AAC41809.1; -.
DR PDB; 1UD4; 05-DEC-01.
DR PDB; 1UD5; 05-DEC-01.
DR PDB; 1UD6; 05-DEC-01.
DR FlyBase; FBgn003691; th.
DR GO; GO:0008189; P:apoptosis inhibitor activity; IDA.
DR GO; GO:0006916; P:anti-apoptosis; IDA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 2.
DR Pfam; PF00097; ZF-C3HC4; 1.
DR SMART; SM00238; BIR; 2.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 2.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat; 3D-structure.
FT REPEAT 44 110
FT REPEAT 226 293
FT REPEAT 391 426
FT ZN_RING
SQ SEQUENCE 438 AA; 48098 MW; A6C22C8EDF5AEF29 CRC64;

Query Match 49.9%; Score 194; DB 1; Length 438;
Best Local Similarity 48.5%; Pred. No. 3.6e-15;
Matches 32; Conservative 14; Mismatches 18; Indels 2; Gaps 1;

QY 3 ARITFTGWIYSVKNK--QLARAGFYALGEGDKVKCFHCGGLTDMKPSDEDWEQHAQVY 60
DB 228 ALRLTFEAWPRLKQKPHQLAEAGFFYTGVDRCVRCSCGGGLMDWNDDEPWEQHALWL 287
QY 61 PGCKYL 66
DB 288 SQCRPV 293

RESULT 15
IAP_GVCP
ID IAP_GVCP STANDARD; PRT; 275 AA.
AC P41436;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis inhibitor IAP.
GN IAP.

```

OS Cydia pomonella granulosus virus (CpGV) (Cydia pomonella
OS Granulovirus).
CC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
OX NCBI_TaxID=28289;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mexican 1;
RX MEDLINE=9318168; PubMed=8445726;
RA Crook N.E., Clem R.J., Miller L.K.;
RT "An apoptosis-inhibiting baculovirus gene with a zinc finger-like
RT motif.";
RL J. Virol. 67:2168-2174(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Mexican 1;
RX MEDLINE=93738577; PubMed=9237352;
RA Kang W., Crook N.E., Winstanley D., O'Reilly D.R.;
RT "Complete sequence and transposon mutagenesis of the BamHI J fragment
RT of Cydia pomonella granulosus virus.";
RL Virus Genes 14:131-136(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Mexican 1;
RX MEDLINE=2144686; PubMed=11562546;
RA Luque T., Finch R., Crook N., O'Reilly D.R., Winstanley D.;
RT "The complete sequence of the Cydia pomonella granulovirus genome.";
RL J. Gen. Virol. 82:2531-2547(2001).
CC -!- FUNCTION: ACTS BY BLOCKING CELLULAR APOPTOSIS RATHER THAN BY
CC PREVENTING VIRAL STIMULATION OF APOPTOSIS.
CC -!- SIMILARITY: Contains 2 BIR repeats.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC -----
DR EMBL; J53466; AAB39098.1; -.
DR PIR; A45679; A45679.
DR HSP; Q13490; IQBH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF0653; BIR; 2.
DR SMART; SMO0238; BIR; 2.
DR SMART; SMO0184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 2.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 7 73 BIR 1.
FT REPEAT 108 175 BIR 2.
FT ZN_FING 228 263 RING-TYPE.
FT SEQUENCE 275 AA; 31290 MW; 84605448869CAD60 CRC64;
Query Match 48.8%; Score 190; DB 1; Length 275;
Best Local Similarity 47.0%; Pred.No. 6.6e-15;
Matches 31; Conservative 12; Mismatches 21; Indels 2; Gaps 1;
QY 3 ARITFGCTWYISVNVK--EQARAGFYALGEGDKVCKPCHGCGGLTDWKPSEDWQCHAKWY 60
DB 110 ARVSHFNWPCMKQRPQEQADAGFTYTGDTNFKCYCDGGLKDWEPEDVPWQHRWF 169
QY 61 PGCKYL 66
DB 170 DRCAYV 175

Search completed: March 10, 2004, 13:53:00
Job time : 10.5 secs

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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:48:59 ; Search time 36 Seconds
(without alignments)
578.450 Million cell updates/sec

Title: US-09-654-743-25
Perfect score: 389
Sequence: 1 YEARIFTGTWYVNVKEQL.....KPSDEPWEQHAQWYCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL 25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	377	96.9	496	11	Q9ESF0	Q9esf0 rattus norv
2	377	96.9	501	11	Q9EQ04	Q9eq04 rattus norv
3	372	95.6	501	11	Q9EQ05	Q9eq05 rattus norv
4	322	82.8	106	4	Q9GRW6	Q9grw6 homo sapien
5	287	73.8	493	13	Q8UWF8	Q8uwf8 gallus gall
6	255	65.6	109	6	Q8RMY4	Q8rmy4 bos taurus
7	216	55.5	405	13	Q8UWH2	Q8uwh2 brachydanio
8	216	55.5	415	13	Q7SXU1	Q7sxu1 brachydanio
9	206	53.0	602	11	Q9ESB9	Q9esb9 rattus norv
10	204	52.4	195	13	Q9IA70	Q9ia70 gallus gall
11	204	52.4	197	13	Q9IA69	Q9ia69 gallus gall
12	204	52.4	610	13	Q57319	Q57319 gallus gall
13	203	52.2	374	11	Q921N0	Q921n0 mus musculu
14	202	51.9	616	13	Q804E2	Q804e2 ictalurus p
15	202	51.9	628	13	Q8UWD2	Q8uwd2 brachydanio
16	202	51.9	647	13	Q7T0K2	Q7t0k2 brachydanio

17	199	51.2	346	5	Q968T8	Q968t8 bombyx mori
18	199	51.2	346	5	Q8IS31	Q8is31 bombyx mori
19	198	50.9	589	11	Q9QZC6	Q9qzc6 rattus norv
20	198	50.9	589	11	Q9ESE8	Q9ese8 rattus norv
21	197	50.6	534	4	Q8IZZ0	Q8izz0 homo sapien
22	196	50.4	283	12	Q80LK8	Q80lk8 adoxophyes
23	195	50.1	283	12	Q80SP4	Q80sf4 hyphantria
24	195	50.1	403	5	Q8WRD9	Q8wrd9 aedes trise
25	194	49.9	438	5	Q9VUX5	Q9vux5 drosophila
26	193	49.6	379	5	Q9U492	Q9u492 trichoplusi
27	192	49.4	261	12	Q9QES9	Q9qes9 epiphyas po
28	192	49.4	377	5	Q9NJ07	Q9nj07 spodoptera
29	189	48.6	255	12	Q7TSS1	Q7tss1 cryptophleb
30	189	48.6	284	12	Q9EN27	Q9en27 anascta moo
31	188	48.3	401	13	Q8JHY9	Q8jhy9 xenopus lae
32	186	47.8	281	12	Q9NLS8	Q9nls8 choristoneu
33	186	47.8	402	5	Q8T621	Q8t621 aedes albop
34	185	47.6	324	13	Q9DDN2	Q9ddn2 gallus gall
35	180.5	46.4	276	12	Q89744	Q89744 buzura supp
36	180	46.3	213	5	Q8MVN1	Q8myn1 boltenia vi
37	178.5	45.9	1403	11	Q8CH68	Q8ch68 mus musculu
38	178.5	45.9	1403	11	Q8CH64	Q8ch64 mus musculu
39	177.5	45.6	597	11	Q9R015	Q9r015 mus musculu
40	177.5	45.6	1402	11	Q8CH65	Q8ch65 mus musculu
41	177.5	45.6	1402	11	Q8CGT4	Q8cgt4 mus musculu
42	177.5	45.6	1402	11	Q8CGT3	Q8cgt3 mus musculu
43	177.5	45.6	1403	11	Q8CH70	Q8ch70 mus musculu
44	177.5	45.6	1403	11	Q8CGT2	Q8cgt2 mus musculu
45	177.5	45.6	1403	11	Q8BG68	Q8bg68 mus musculu

ALIGNMENTS

RESULT 1

Q9ESF0 PRELIMINARY; PRT; 496 AA.

AC Q9ESF0;

DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Inhibitor of apoptosis protein 3.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;

RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of Apoptosis Protein 1, 2, and 3 Genes."

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

DR EMBL; AF183429; AAG22969.1; -.

DR HSP; P98170; I03P.

DR GO; GO:0005622; C:intracellular; IEA.

DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.

DR GO; GO:0006916; F:anti-apoptosis; IEA.

DR InterPro; IPR001370; BIR.

DR InterPro; IPR001841; Znf_ring.

DR Pfam; PF00653; BIR; 3.

DR SMART; SM00238; BIR; 3.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01282; BIR_REPEAT_1; 3.

DR PROSITE; PS01443; BIR_REPEAT_2; 3.

DR PROSITE; PS00089; ZF_RING_2; 1.

KW Metal-binding; Zinc; Zinc-finger.

SQ SEQUENCE 496 AA; 56117 MW; 9BEF142AAEC5B798 CRC64;

Query Match 96.9%; Score 377; DB 11; Length 496;

Best Local Similarity 95.5%; Pred. No. 2.3e-34;

Matches 63; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 YEARIFTGWTIYSVKNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQAKWY 60
Db 264 YDARIIVTGTWLYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQAKWY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 2
Q9EQ04 PRELIMINARY; PRT; 501 AA.
AC Q9EQ04;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 3.
DE Rattus norvegicus (Rat)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Ovary;
RA Lareu R.R., Bradley C.K., Lacher M., Friis R.R., Dharmarajan A.M.;
RT "Cloning, characterization and regulation of an inhibitor of apoptosis
RL protein in the rat corpus luteum."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF304334; AAG41193.1; -.
DR HSSP; P98170; IG3F.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 501 AA; 56578 MW; 4863869F2E0C8CD CRC64;

Query Match 96.9%; Score 377; DB 11; Length 501;
Best Local Similarity 95.5%; Pred. No. 2.3e-34;
Matches 63; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIFTGWTIYSVKNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQAKWY 60
Db 264 YDARIIVTGTWLYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQAKWY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 3
Q9EQ05 PRELIMINARY; PRT; 501 AA.
AC Q9EQ05;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 3.
DE Rattus norvegicus (Rat)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Ovary;
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RA Lareu R.R., Bradley C.K., Lacher M., Friis R.R., Dharmarajan A.M.;
RT "Cloning, characterization and regulation of an inhibitor of apoptosis
RL protein in the rat corpus luteum."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF304333; AAG41192.1; -.
DR HSSP; P98170; IG3F.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 501 AA; 56548 MW; 0973F8F28E81CSA0 CRC64;

Query Match 95.6%; Score 372; DB 11; Length 501;
Best Local Similarity 93.9%; Pred. No. 8.6e-34;
Matches 62; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFTGWTIYSVKNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQAKWY 60
Db 264 YDARIIVTGTWLYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQAKWY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 4
Q96RW6 PRELIMINARY; PRT; 106 AA.
AC Q96RW6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE TAP-like protein 3.
GN ILP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mir S.S., Duckett C.S.;
RT "Molecular cloning of human homologs of IAP-like protein."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF164681; AAK81891.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 1.
SQ SEQUENCE 106 AA; 12360 MW; 68BAD3A8A880A891 CRC64;

Query Match 82.8%; Score 322; DB 4; Length 106;
Best Local Similarity 94.6%; Pred. No. 7.4e-29;
Matches 53; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 WIYSVKNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQAKWY PGCKYL 66
Db 2 WIYSVKNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQAKWY PGCKYL 57

RESULT 5
Q8UVF8
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ID Q8UVF8 PRELIMINARY; PRT; 493 AA.
AC Q8UVF8;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 3.
GN IAP3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RA Brigham J.T., Johnson A.L.;
RT "Identification of chicken inhibitor of apoptosis protein XIAP
  (IAP3).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF451854; AAL47170.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0089; ZF_RING_2; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 493 AA; 55251 MW; 030A9F56CB6119BC CRC64;

Query Match 73.8%; Score 287; DB 13; Length 493;
Best Local Similarity 71.2%; Pred. No. 3.6e-24;
Matches 47; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 YEARIFTGTWYISVNVKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPEQHAQWY 60
DB 264 YERRIQTLAWIYPVNVKEHLAEGYSTGNGDHVVCVFCGGLQEWKENDPDWDQAKWF 323
QY 61 PGCKYL 66
DB 324 PGCKFL 329

RESULT 6
Q8WMT4 PRELIMINARY; PRT; 109 AA.
AC Q8WMT4;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE X-linked inhibitor of apoptosis protein (Fragment).
GN XIAP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_TaxID=9913;
RP SEQUENCE FROM N.A.
RA Gutierrez-Adan A., Madrid-Bury N., Arroyo-Garcia R., Fernandez R.,
RA Jimenez A., Pintado B., De la Fuente J.;
RT "Hyperglycemia-induced apoptosis affects sex ratio of preimplantation
  embryos.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF458770; AAL66179.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
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DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 2.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 12361 MW; C4027DC88213DB6D CRC64;

Query Match 65.6%; Score 255; DB 6; Length 109;
Best Local Similarity 91.7%; Pred. No. 2.9e-21;
Matches 44; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFTGTWYISVNVKEQLARAGFYALGEGDKVKCFHCGGGLTDWKP 48
DB 57 YEARIIFTGTWYISVNVKEQLARAGFYALGEGDKVQCFCGGLNDWKP 104

RESULT 7
Q8UWH2 PRELIMINARY; PRT; 405 AA.
AC Q8UWH2;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE XIAP.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]_TaxID=7955;
RP SEQUENCE FROM N.A.
RA MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
  zebrafish.";
RL Cell Death Differ. 7:509-510(2000).
RN [2]_TaxID=7955;
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF439767; AAL32047.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 405 AA; 45564 MW; A366E342D83BECAB CRC64;

Query Match 55.5%; Score 216; DB 13; Length 405;
Best Local Similarity 53.0%; Pred. No. 3.1e-16;
Matches 35; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 1 YEARIFTGTWYISVNVKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPEQHAQWY 60
DB 229 FEGRLDSFKGRQHPIDPERLARAGFYSTGQDRVYMCFCGCGVKAMWPDPEEHAHY 288
QY 61 PGCKYL 66
DB 289 PGCKFL 294

RESULT 8
Q7SXU1 PRELIMINARY; PRT; 415 AA.
ID Q7SXU1
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RT Apoptosis Protein 1, 2, and 3 Genes."
Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR HSSP; AF183430; AAG22970.1; -.
DR HSP; Q13490; IQBH.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA..
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; ZnF_fing.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 602 AA; 67326 MW; CC91385EEA62DE5A CRC64;

Query Match          53.0%; Score 206; DB 11; Length 602;
Best Local Similarity 52.9%; Pred.No.6.se-15;
Matches 36; Conservative 10; Mismatches 20; Indels 2; Gaps 1;

QY      1 YEARIFFGFWIWS--VNKEQLARAGFYALRGSDKVKCFHCGGGGLTDWKPSDPEQHAK 58
Db      255 HAARVRFSTWPSALVHPQLASAGFYTHGSHDDVKCFCDGGLRWESGDPPWEHAK 314
               |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      59 WYPCKYL 66
Db      315 WFPRCYL 322

RESULT 10
Q9IA70 PRELIMINARY; PRT; 195 AA.
ID Q9IA70 AC
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-JUN-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RC STRAIN=breed Leghorn; TISSUE=Spleen;
RX MEDLINE=21158006; PubMed=11261557;
RA Zhou H., Liu W., Lamont S.J.;
RT "Genetic variation among chicken lines and mammalian species in
   specific genes.";
RL Poult. Sci 80:284-288(2001).
DR EMBL; AF221082; AAF35319.1; -.
DR HSSP; Q13490; IQBH.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 2.
FT NON TER 1
FT NON TER 195
SQ SEQUENCE 195 AA; 22347 MW; 9C39BFA75E24E48 CRC64;

Query Match          52.4%; Score 204; DB 13; Length 195;

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Best Local Similarity 54.4%; Pred. No. 3.3e-15;
Matches 37; Conservative 8; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEAR1FTGTW--IYSVNKEOLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWEQHAH 58
DB 116 HEARVKTFINWFTPIPVQPEGLADAGFYVGRNDVVKFCFCCDGLRCWESGDDPWIEHAK 175
QY 59 WYPGCKYL 66
DB 176 WFPCEYL 183

RESULT 11
Q91A69 PRELIMINARY; PRT; 197 AA.
AC Q91A69;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=breed Fayoumi; TISSUE=Spleen;
RX MEDLINE=21158006; PubMed=11261557;
RA Zhou H., Liu W., Lamont S.J.;
RT "Genetic variation among chicken lines and mammalian species in
specific genes.";
RL Poul. Sci. 80:284-288(2001).
DR EMBL; AF221083; AAF35320.1; .
DR HSSP; Q13490; IQBH.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0008916; F:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 2.
FT NON_TER 1
FT TER 197
SQ SEQUENCE 197 AA; 22602 MW; D7923DABCF623E1A CRC64;

Query Match 52.4%; Score 204; DB 13; Length 197;
Best Local Similarity 54.4%; Pred. No. 3.3e-15;
Matches 37; Conservative 8; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEAR1FTGTW--IYSVNKEOLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWEQHAH 58
DB 117 HEARVKTFINWFTPIPVQPEGLADAGFYVGRNDVVKFCFCCDGLRCWESGDDPWIEHAK 176
QY 59 WYPGCKYL 66
DB 177 WFPCEYL 184

RESULT 12
O57319 PRELIMINARY; PRT; 610 AA.
AC O57319;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis PROTEIN 1 (IAP) (Inhibitor of T cell apoptosis
PROTEIN).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN; TISSUE=EMBRYONIC FIBROBLAST;
RX MEDLINE=98038801; PubMed=9372964;
RA You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;
RT "ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a
mediator of the antiapoptotic activity of the v-rel oncoprotein.";
RL Mol. Cell. Biol. 17:7328-7341(1997)
CC -1- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED
CELLS.
CC -1- SUBCELLULAR LOCATION: EXPRESSED PREDOMINANTLY IN THE CYTOPLASM OF
THE V-REL-TRANSFORMED CELLS.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN THE
SPLEEN, THYMUS, BURSA, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS
IN TESTIS, BRAIN, AND SKELETAL MUSCLE.
CC -1- INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION
PROCESS.
CC -1- DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC EFFECT.
CC -1- SIMILARITY: MEMBER OF THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION OF
APOPTOSIS PROTEIN REPEAT).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL; AF008592; AAB88044.1; .
DR HSSP; Q13490; IQBH.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0008916; F:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf_C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 30 97 BIR_REPEAT 1.
FT REPEAT 176 242 BIR_REPEAT 2.
FT REPEAT 262 329 BIR_REPEAT 3.
FT ZN_FING 563 597 C3HC4-TYPE.
SQ SEQUENCE 610 AA; 68924 MW; ADF47619650B44A6 CRC64;

Query Match 52.4%; Score 204; DB 13; Length 610;
Best Local Similarity 54.4%; Pred. No. 1.1e-14;
Matches 37; Conservative 8; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEAR1FTGTW--IYSVNKEOLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWEQHAH 58
DB 262 HEARVKTFINWFTPIPVQPEGLADAGFYVGRNDVVKFCFCCDGLRCWESGDDPWIEHAK 321
QY 59 WYPGCKYL 66
DB 322 WFPCEYL 329

RESULT 13
Q921N0 PRELIMINARY; PRT; 374 AA.
AC Q921N0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Similar to baculoviral IAP repeat-containing 2.
GN BIRC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CN NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011338; AAH11338.1; -
DR MGD; MGI:1197007; Birc2.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
SQ SEQUENCE 374 AA; 41915 MW; 1D2B54C32D7E46F3 CRC64;

Query Match 52.2%; Score 203; DB 11; Length 374;
Best Local Similarity 52.9%; Pred. No. 8.6e-15;
Matches 36; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIFTGWTW--YVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPWEQAKW 58
DB 253 HAARIRFSNWPSSALVHSQELASAGFYVTGHSDDVKCFCCDGLRCWESGDDPWEHAKW 312
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QY 59 YPGCKYL 66
DB 313 WFPCEYL 320
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RESULT 14
Q804E2 PRELIMINARY; PRT; 616 AA.
ID Q804E2;
AC Q804E2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Inhibitor of apoptosis protein-1.
GN CIAP-1.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
[1]
RP SEQUENCE FROM N.A.
RA Praveen K., Leary J.H. III, Evans D.L., Jaso-Friedmann L.;
RT "Cloning of anti-apoptotic genes in non-specific cytotoxic cells."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV184377; AAO24632.1; -
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
SQ SEQUENCE 616 AA; 69546 MW; D1389D915C6B256 CRC64;

Query Match 51.9%; Score 202; DB 13; Length 616;
Best Local Similarity 52.2%; Pred. No. 1.9e-14;
Matches 35; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 2 YEARIFTGWTW--IYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPWEQAKW 59
DB 270 EERLLTFVNWPARIIPVRPDLAKAGFYVYGRNDDVKCFCCDGLRCWESGDDPWEHAKW 329
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QY 60 YPGCKYL 66
DB 330 FPRCEYL 336
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RESULT 15
Q8UWD2 PRELIMINARY; PRT; 628 AA.
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AC Q8UWD2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Iap1.
GN IAP1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
[1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20373792; PubMed=10917738;
EX Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish."
RT Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF442500; AAU33679.1; -
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; ZF-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 628 AA; 70098 MW; 5B68CEB6A87C8A95 CRC64;

Query Match 51.9%; Score 202; DB 13; Length 628;
Best Local Similarity 52.2%; Pred. No. 1.9e-14;
Matches 35; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 2 YEARIFTGWTW--IYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPWEQAKW 59
DB 280 EERLLTFVNWPSPRIIPVRPDLAKAGFYVYGRNDDVKCFCCDGLRCWESGDDPWEHAKW 339
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QY 60 YPGCKYL 66
DB 340 FPRCEYL 346
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Search completed: March 10, 2004, 13:54:25
Job time : 36 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 13, 2004, 00:37:57 ; Search time 1045.5 Seconds
(without alignments)
8208.437 Million cell updates/sec

Title: US-09-654-743-47

Perfect score: 198

Sequence: 1 tatgaagcagcgtattac.....atccagggtgcaaatatctg 198

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Result No.	Score	Match	Length	DB ID	Description
1	198	100.0	1588	6	AR263641 Sequence
2	198	100.0	1659	6	E31042 Method for
3	198	100.0	1659	6	AR270490 Sequence
4	198	100.0	1659	9	U32974 Human IAP-1
5	198	100.0	2086	9	BC032729 Homo sapi
6	198	100.0	2404	6	AX429575 Sequence
7	198	100.0	2540	6	AR103281 Sequence
8	198	100.0	2540	6	AR302736 Sequence
9	198	100.0	2540	6	AR380355 Sequence
10	198	100.0	2540	6	AR435471 Sequence
11	198	100.0	2540	6	AX412118 Sequence
12	198	100.0	2540	6	AX587804 Sequence
13	198	100.0	3000	9	HSU45880 Sequence
14	198	100.0	5232	6	AX412131 Sequence
15	198	100.0	5232	6	AR106397 Sequence
16	198	100.0	5232	6	AR116699 Sequence
17	198	100.0	5232	6	AR370617 Sequence
18	198	100.0	5232	6	AX670900 Sequence
19	198	100.0	5232	6	BD190868 Defection
20	180.4	91.1	1752	6	AX104956 Sequence
21	180.4	91.1	1752	9	AF164681 Homo sapi
22	180.4	91.1	154214	9	AC079753 Sequence
23	179.4	90.6	1491	10	AF183429 Rattus no
24	179.4	90.6	2468	10	AB033366 Rattus no
25	179.4	90.6	3032	10	AF304334 Rattus no
26	177.8	89.8	2032	10	AF304333 Rattus no
27	174.6	88.2	1988	10	MMU36842 Mus musculu
28	173	87.4	2100	6	AR302739 Sequence
29	173	87.4	2100	6	AF435474 Sequence
30	173	87.4	2100	6	AX412124 Sequence
31	169.8	85.8	2691	6	AR106400 Sequence
32	169.8	85.8	2691	6	AR116702 Sequence
33	169.8	85.8	2691	6	AR370620 Sequence
34	169.8	85.8	2691	6	AX670906 Sequence
35	169.8	85.8	2691	6	BD190871 Defection
36	169.8	85.8	205991	2	MMU88990
37	169.8	85.8	205991	2	AC109227 Mus muscu
38	169.8	85.8	208236	2	AC137152 Mus muscu
39	166	83.8	711	6	AX104970 Sequence
40	166	83.8	711	9	AY030052 Pan trogl
41	166	83.8	1758	6	AX370787 Sequence
42	166	83.8	1758	6	AX370789 Sequence
43	166	83.8	4993	6	AX104968 Sequence
44	166	83.8	4993	9	AF164682 Homo sapi
45	166	83.8	144301	9	AC010467 Homo sapi

ALIGNMENTS

RESULT 1
AR263641
LOCUS AR263641 1588 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 3 from patent US 6331412.
ACCESSION AR263641
VERSION AR263641.1 GI:28075567
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1588)
AUTHORS Korneluk, R.G. and Lagace, M.
TITLE Methods and compounds for modulating male fertility
JOURNAL Patent: US 6331412-A 3 18-DEC-2001;
FEATURES Location/Qualifiers

Pred. No. is the number of results predicted by chance to have a

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Best Local Similarity 100.0%; Pred. No. 2.7e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATCTCAGTTAAAGAGGAGCTT 60
DB 826 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATCTCAGTTAAAGAGGAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGCCAGTCAAGACCCCTTGGGACAAACATGCTAAATGGTAT 120
DB 886 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGCCAGTCAAGACCCCTTGGGACAAACATGCTAAATGGTAT 945

QY 121 GGAGGCTTAACCTGATTTGAAGCCAGTCAAGACCCCTTGGGACAAACATGCTAAATGGTAT 180
DB 946 GGAGGCTTAACCTGATTTGAAGCCAGTCAAGACCCCTTGGGACAAACATGCTAAATGGTAT 1005

QY 181 CCAGGCTGCAAAATATCTG 198
DB 1006 CCAGGCTGCAAAATATCTG 1023

RESULT 2
E31042
LOCUS      E31042
DEFINITION Method for screening substance inhibiting binding to XIAP.
ACCESSION E31042
VERSION    E31042.1 GI:13017307
KEYWORDS  JP 199326328-A/2.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE 1 (bases 1 to 1659)
AUTHORS   Kunihiro,M.
TITLE     Method for screening substance inhibiting binding to XIAP
JOURNAL   KUNIHIRO MATSUMOTO
COMMENT   OS Unidentified
          PN JP 199326328-A/2
          PD 26-NOV-1999
          PF 13-MAY-1998 JP 1998130378
          PR KUNIHIRO MATSUMOTO
          PI G01N33/536,A61K38/00,A61K38/00,A61K38/00,A61K38/22,
          PC A61K39/395,
          PC A61K45/00,A61K45/00,A61K45/00,C07K7/06,C07K14/47,-PC
          PC G01N33/536,
          G01N33/536,G01N33/536//C12N15/09,C12P21/09,A61K37/02,A61K37/02,PC
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          PC A61K37/02,A61K37/24,C12N15/00
          CC Strandedness: Double;
          CC Topology: Linear;
          FH Key Location/Qualifiers
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FEATURES
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Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 874 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATCTCAGTTAAAGAGGAGCTT 933

RESULT 3
AR270490
LOCUS      AR270490
DEFINITION Sequence 1053 from patent US 6500938.
ACCESSION AR270490
VERSION    AR270490.1 GI:29701724
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE 1 (bases 1 to 1659)
AUTHORS   Au-Young,J. and Seilhamer,J.J.
TITLE     Composition for the detection of signaling pathway gene expression
JOURNAL   Patent: US 6500938-A 1053 31-DEC-2002;
          Location/Qualifiers
FEATURES   1..1659
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          /mol_type="genomic DNA"

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Best Local Similarity 100.0%; Pred. No. 2.7e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 874 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATCTCAGTTAAAGAGGAGCTT 933

QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGCCAGTCAAGACCCCTTGGGACAAACATGCTAAATGGTAT 120
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QY 121 GGAGGCTTAACCTGATTTGAAGCCAGTCAAGACCCCTTGGGACAAACATGCTAAATGGTAT 180
DB 994 GGAGGCTTAACCTGATTTGAAGCCAGTCAAGACCCCTTGGGACAAACATGCTAAATGGTAT 1053

QY 181 CCAGGCTGCAAAATATCTG 198
DB 1054 CCAGGCTGCAAAATATCTG 1071

RESULT 4
HSU32974
LOCUS      HSU32974
DEFINITION Human IAP-like protein ILP mRNA, complete cds.
ACCESSION U32974
VERSION    U32974.1 GI:1016687
KEYWORDS   apoptosis; ring finger; zinc finger.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 1659);
REFERENCE 1 (bases 1 to 1659);
AUTHORS   Duckett,C.S., Nava,V.E., Gedrich,R.W., Clem,R.J., Van Dongen,J.L.,
          Giffillan,M.C., Shiels,H., Hardwick,J.M. and Thompson,C.B.
TITLE     A conserved family of cellular genes related to the baculovirus iap
          gene and encoding apoptosis inhibitors
JOURNAL   EMBO J. 15 (11), 2685-2694 (1996)
MEDLINE   96256286

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TITLE Mammalian IAP gene family, primers, probes and detection methods
JOURNAL Patent: US 6541457-A 3 01-APR-2003;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"

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Query Match 100.0%; Score 198; DB 6; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.6e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 60
DB 826 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGTGATAAAGTAAAGTCTTTCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGTGATAAAGTAAAGTCTTTCACTGTGGA 945

QY 121 GGAGGGCTAACTGATTGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
DB 946 GGAGGGCTAACTGATTGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAAAATATCTG 198
DB 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 9
AR380355 2540 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 900 from patent US 6607879.
DEFINITION
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
TITLE Compositions for the detection of blood cell and immunological response gene expression
JOURNAL Patent: US 6607879-A 900 19-AUG-2003;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.6e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 GGAGGGCTAACTGATTGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
DB 946 GGAGGGCTAACTGATTGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAAAATATCTG 198
DB 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 10
AR435471 2540 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 3 from patent US 6656704.
DEFINITION
AUTHORS Korneluk,R.G., MacKenzie,A.E., Baird,S. and Liston,P.
TITLE Mammalian apoptosis inhibitor protein gene family, primers, probes and detection methods
JOURNAL Patent: US 6656704-A 3 02-DEC-2003;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.6e-44;
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DB 946 GGAGGGCTAACTGATTGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAAAATATCTG 198
DB 1006 CCAGGGTGCAAAATATCTG 1023

LOCUS AR435471 2540 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 3 from patent US 6656704.
ACCESSION AR435471
VERSION AR435471.1 GI:40198322
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2540)
AUTHORS Korneluk,R.G., MacKenzie,A.E., Baird,S. and Liston,P.
TITLE Mammalian apoptosis inhibitor protein gene family, primers, probes and detection methods
JOURNAL Patent: US 6656704-A 3 02-DEC-2003;
FEATURES Location/Qualifiers
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QY 121 GGAGGGCTAACTGATTGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
DB 946 GGAGGGCTAACTGATTGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAAAATATCTG 198
DB 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 11
AX412118 2540 bp DNA linear PAT 14-JUN-2002
LOCUS Sequence 218 from Patent WO0226968.
DEFINITION
ACCESSION AX412118
VERSION AX412118.1 GI:21444581
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.
TITLE Antisense iap nucleic acids and uses thereof
JOURNAL Patent: WO 0226968-A 218 04-APR-2002;
UNIVERSITY University of Ottawa (CA); Aegera Therapeutics Inc. (CA)
FEATURES Location/Qualifiers
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QY 181 CCAGGGTGAATATCTG 198

Db 1006 CCAGGGTGAATATCTG 1023

RESULT 12

AX587804

LOCUS AX587804 2540 bp DNA linear PAT 10-JAN-2003

DEFINITION Sequence 274 from Patent WO0246467.

ACCESSION AX587804

VERSION AX587804.1 GI:28212417

KEYWORDS synthetic construct

ORGANISM synthetic construct

SOURCE artificial sequences.

REFERENCE 1

AUTHORS Bertucci, F., Houlgatte, R., Birnbaum, D., Nguyen, C., Viens, P. and Fert, V.

TITLE Gene expression profiling of primary breast carcinomas using arrays of candidate genes

JOURNAL Patent: WO 0246467-A 274 13-JUN-2002;

IPSOGEN (FR)

FEATURES

Location/Qualifiers

1..2540

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="primer"

misc_feature 1..2540

/note="baculoviral iap repeat-containing 4 (BIRC4) gene."

ORIGIN

Query Match 100.0%; Score 198; DB 6; Length 2540;

Best Local Similarity 100.0%; Pred. No. 2.6e-44;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTTACTTTTGGACATGGATATCTCAGTTAAAGGAGCAGCTT 60

Db 826 TATGAAGCAGGATCTTTACTTTTGGACATGGATATCTCAGTTAAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120

Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 945

QY 121 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180

Db 946 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGAATATCTG 198

Db 1006 CCAGGGTGAATATCTG 1023

RESULT 13

HSU45880

LOCUS HSU45880 2540 bp mRNA linear PRI 16-FEB-1996

DEFINITION Human X-linked inhibitor of apoptosis protein XIAP mRNA, complete cds

ACCESSION U45880

VERSION U45880.1 GI:1184319

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2540)

AUTHORS Liston, P., Roy, N., Tamai, K., Lefebvre, C., Baird, S.,

Cherton-Horvat, G., Farahani, R., McLean, M., Ikeda, J., Mackenzie, A. and Korneluk, R.G.

Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes

JOURNAL Nature 379 (6563), 349-353 (1996)

MEDLINE 96149249

PUBMED 8552191

REFERENCE 2 (bases 1 to 2540)

AUTHORS Baird, S.D.

TITLE Direct Submission

JOURNAL Submitted (16-JAN-1996) Stephen D. Baird, Children's Hospital of Eastern Ontario, Genetics, 401 Smyth Rd., Ottawa, Ontario, K1H 8L1, Canada

FEATURES

Location/Qualifiers

1..2540

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/map="xq24-25"

/tissue type="brain"

/clone_lib="Stratagene lambdazap-II human fetal brain"

/dev stage="fetal"

34..1527

/function="inhibition of apoptosis"

/note="XIAP"

/codon_start=1

/evidence=experimental

/product="X-linked inhibitor of apoptosis protein"

/protein_id="AAC50373.1"

/db_xref="GI:1184320"

/translation="MTFNSPEGSKTCVPADINKEREFVEFNRLLKTFANFPSPGSPVSA

STLQAGFLYTGEGDVTVCFSCHAAVDNRWQYSDSAVGRHKVSPNCRFLNGFYLENSA

TOSTNGIQNGYKVENYLGSRDHFALDRPSETHADYLRLTQGVNDISITVIRNPAM

YCEARLKSPQNPEDYLAHLTRELASAGLYTTGIGDQVQFCGCGKLNWPCEDRAWS

EHRHPNCFPVLRNLINRSDASVLYNFPNPNFNSMADYARIITFTGTWI

YSVVKELARAGFALGCEKVKCFKCGGLTDWKPSEDWEOHAKWYPCGYLLBQK

GOEYNNHILHSLECLVETKTSPLTRIDDTIFONPQVEATRMGFSKDIKKI

MEKIOISGNYKSELEVLDVADLYNAOKDSMQDESSQTSLOKELISEQLRLQEEKLC

KICMDRIALVFPVPCGHLVTCQCAENVKCPMCYIVITFKQKIFMS"

misc_feature 108..309

/note="encodes BIR1 (Baculovirus IAP Repeat)"

misc_feature 520..723

/note="encodes BIR2"

misc_feature 826..1020

/note="encodes BIR3"

misc_feature 1381..1495

/note="encodes Ring Zinc Finger"

ORIGIN

Query Match 100.0%; Score 198; DB 9; Length 2540;

Best Local Similarity 100.0%; Pred. No. 2.6e-44;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTTACTTTTGGACATGGATATCTCAGTTAAAGGAGCAGCTT 60

Db 826 TATGAAGCAGGATCTTTACTTTTGGACATGGATATCTCAGTTAAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120

Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 945

QY 121 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180

Db 946 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGAATATCTG 198

Db 1006 CCAGGGTGAATATCTG 1023

RESULT 14

AX412131

LOCUS AX412131 3000 bp DNA linear PAT 14-JUN-2002

DEFINITION Sequence 231 from Patent WO0226968.

ACCESSION AX412131

VERSION AX412131.1 GI:21444588

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.

AUTHORS Antisense iap nucleic acids and uses thereof

TITLE Patent: WO 0226968-A 231 04-APR-2002;

JOURNAL University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)

FEATURES Location/Qualifiers

1..3000

source /organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 198; DB 6; Length 3000;
Best Local Similarity 100.0%; Pred. No. 2.5e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATACTACGTTAACAGGAGCAGCTT 60
DB 1482 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATACTACGTTAACAGGAGCAGCTT 1541
QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATATAAGTAAAGTGCCTTTCACTGTGGA 120
DB 1542 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATATAAGTAAAGTGCCTTTCACTGTGGA 1601
QY 121 GGAGGGCTAACTGATGTAAGCCGACGACCCCTTGGGACCAACATGCTAAATGGTAT 180
DB 1602 GGAGGGCTAACTGATGTAAGCCGACGACCCCTTGGGACCAACATGCTAAATGGTAT 1661
QY 181 CCAGGGTGCAATATCTG 198
DB 1662 CCAGGGTGCAATATCTG 1679

RESULT 15

AR106397

LOCUS 5232 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 3 from patent US 6107041.

ACCESSION AR106397

VERSION AR106397.1 GI:12820927

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 5232)

AUTHORS Korneluk,R.G., MacKenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and

Pratt,C.

TITLE Detection and modulation of IAPs for the diagnosis and treatment of

proliferative disease

JOURNAL Patent: US 6107041-A 3 22-AUG-2000;

FEATURES Location/Qualifiers

1..5232

source /organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 198; DB 6; Length 5232;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATACTACGTTAACAGGAGCAGCTT 60
DB 826 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATACTACGTTAACAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATATAAGTAAAGTGCCTTTCACTGTGGA 120

Db 886 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATATAAGTAAAGTGCCTTTCACTGTGGA 945
QY 121 GGAGGGCTAACTGATTTGGGAGCCCGACGTTGAAGACCCCTTGGGACCAACATGCTAAATGGTAT 180
DB 946 GGAGGGCTAACTGATTTGGGAGCCCGACGTTGAAGACCCCTTGGGACCAACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAAAATATCTG 198
DB 1006 CCAGGGTGCAAAATATCTG 1023

Search completed: March 13, 2004, 05:11:48
Job time : 1051.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 12, 2004, 21:10:12 ; Search time 265 Seconds
(without alignments)
3174.125 Million cell updates/sec

Title: US-09-654-743-47
Perfect score: 198
Sequence: 1 tatgaagcagcgatctttac.....atccagggtgcaaatatctg 198

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 337863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 29Jan04: *
1: geneseqn1980s: *
2: geneseqn1990s: *
3: geneseqn2000s: *
4: geneseqn2001as: *
5: geneseqn2001bs: *
6: geneseqn2002as: *
7: geneseqn2003as: *
8: geneseqn2003bs: *
9: geneseqn2003cs: *
10: geneseqn2004as: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	100.0	1588	6	AB52803 DNA encod
2	198	100.0	1559	3	AAA06940
3	198	100.0	1559	6	ABK13197 Human tes
4	198	100.0	1559	6	AB52802 DNA encod
5	198	100.0	2404	6	AAK99405 DNA of AP
6	198	100.0	2540	2	AAAT70836 Human apo
7	198	100.0	2540	3	AAA64901 Human X-1
8	198	100.0	2540	6	ABK93869 Human cdn
9	198	100.0	2540	6	ABV94283 Breast ca
10	198	100.0	2540	7	AAU53731 X-linked
11	198	100.0	2540	8	AD81002 RING-SH c
12	198	100.0	3000	6	ABK93875 Human cdn
13	198	100.0	5232	2	AAV55038 Human XIA
14	180.4	91.1	1752	4	AAAD03575 Human IAP
15	174.6	88.2	1988	2	AAAT72710 Mouse inh
16	173	87.4	2100	2	AAAT70839 Mouse apo
17	173	87.4	2100	6	ABK93872 Mouse cdn
18	169.8	85.8	2691	2	AAV55041 Murine XI
19	169.8	85.8	2691	4	AB528102 Chimpanze
20	166	83.8	711	4	AAAD03582 Human inh
21	166	83.8	1758	6	ABK14678 Human inh
22	166	83.8	1758	6	ABK14677 Human inh
23	165	83.8	4993	4	AAAD03581 Human IAP

24	164.4	83.0	711	3	AAA06940	AA06940 DNA encod
25	164.4	83.0	1559	6	ABK13197	Abk13197 Human tes
26	164.4	83.0	1559	6	AB52802	AB52802 DNA encod
27	162.8	82.2	711	4	AAAD03583	Aad03583 Gorilla I
c	157.8	79.7	578	2	AAAX02960	Aax02960 Human IL-
28	157.8	79.7	578	2	AAAX02960	Aax02960 Human IL-
29	131.4	66.4	802	2	AAAX03018	Aax03018 Human IL-
c	96.8	48.9	302	6	ABQ58785	Abq58785 Human col
30	96.8	48.9	302	6	ABQ58785	Abq58785 Human col
31	83	41.9	1402	2	AAAX03028	Aax03028 Human IL-
32	78.6	39.7	2563	7	ACA56478	Aca56478 Human sig
33	78.6	39.7	2563	8	ADB80989	Adb80989 RING-SH c
34	78.6	39.7	2601	2	AAAT61591	Aat61591 Human c-I
35	78.6	39.7	2666	2	AAAT70837	Aat70837 Human apo
36	78.6	39.7	2676	6	ABK93870	Abk93870 Human cdn
37	78.6	39.7	3076	2	AAAT72712	Aat72712 Human inh
38	78.6	39.7	3076	2	AAZ41005	Aaz41005 Human cel
39	78.6	39.7	3076	2	AAZ22096	Aaz22096 Human cel
40	78.6	39.7	3076	6	ABL62746	Ab162746 Breast ca
41	78.6	39.7	3076	6	ABL66325	Ab166325 Lung canc
42	78.6	39.7	3076	7	ABX10968	Abx10968 CDNA enco
43	78.6	39.7	3076	9	AAAD60472	Aad60472 Human cel
44	78.6	39.7	3153	7	ABZ58104	Abz58104 Inhibitor
45	78.6	39.7	3164	7	ABV75363	Abv75363 Human CIA

ALIGNMENTS

RESULT 1
ABS52803
ID ABS52803 standard; DNA; 1588 BP.

XX ABS52803;

XX 15-NOV-2002 (first entry)

XX DNA encoding X-linked inhibitor of apoptosis, XIAP.

XX Inhibitor of apoptosis protein; IAP; testis; XIAP; apoptosis; TIAP;

KW fertility; testicular cancer; male infertility; male birth control;

KW X-linked inhibitor of apoptosis; gene; ds.

OS Mammalia.

XX Key Location/Qualifiers

FT CDS 34..1527

FT /tag= a

FT /transl_except= (pos:34..36, aa:Xaa)

FT /product= "X-linked inhibitor of apoptosis protein, XIAP"

FT /partial

FT /note= "Start codon illegible in specification;

FT represented as nnn"

FT US2002086409-A1.

PD 04-JUL-2002.

XX 18-DEC-2001; 2001US-00024433.

XX 29-JAN-1998; 98US-0073001P.

XX 29-JAN-1999; 99US-00239867.

XX (KORN/) KORNELUK R G.

XX (LAGA/) LAGACE M.

XX Korneluk RG, Lagace M;

XX MPI; 2002-642245/69.

XX P-PSDB; ABG32418.

XX Novel polypeptide, a member of apoptosis family of proteins

PT that is expressed in testes useful for modulating apoptosis in cells,

PT particular cells involved in male fertility.

PS Example 3; Fig 4A; 24pp; English.

XX A substantially pure TIAP polypeptide (I), a member of IAP (inhibitor of
CC apoptosis) family of proteins that is expressed in the testes. (I) is
CC useful for identifying a compound that modulates TIAP biological activity
CC (I) is useful for increasing apoptosis in a cell, preferably a germ-line
CC cell and for increasing fertility in an animal. (I) is useful for
CC treating or preventing apoptosis which occurs as a part of testicular
CC cancer and male infertility. TIAP may be manipulated for use as a male
CC birth control. TIAP polypeptides and nucleic acid sequences also have
CC diagnostic use in the detection or monitoring of conditions involving
CC aberrant levels of apoptosis. The present sequence represents the coding
CC sequence of X-linked inhibitor of apoptosis (XIAP)

XX SQ Sequence 1588 BP; 505 A; 274 C; 359 G; 444 T; 0 U; 6 Other;

Query Match 100.0%; Score 198; DB 6; Length 1588;
Best Local Similarity 100.0%; Pred. No. 3e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGACGACGGATCTTACTTTTGGACATGGATATCTCAGTTAAACAAGGCGCGCTT 60
DB 826 TATGACGACGGATCTTACTTTTGGACATGGATATCTCAGTTAAACAAGGCGCGCTT 885
QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATATAAGTAAAGTCTTCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATATAAGTAAAGTCTTCACTGTGGA 945
QY 121 GGAGGGCTTAAGTGGAGCCCGAGTGAAGACCTTTGGACACATGCTAAATGGTAT 180
DB 946 GGAGGGCTTAAGTGGAGCCCGAGTGAAGACCTTTGGACACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAAAATATCTG 198
DB 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 2

AZ48862
ID AA248862 standard; cDNA; 1659 BP.

XX AC AA248862;

XX DT 24-MAR-2000 (first entry)

XX DE Human XIAP coding sequence.

XX KW Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
KW transforming growth factor-beta activated kinase 1; monocyte migration;
KW TAK1 binding protein 1; extracellular matrix protein production;
KW cell growth inhibitor; beta-amyloid protein deposition;
KW immunosuppression; Transforming growth factor-beta; ds.

XX OS Homo sapiens.

XX PN JP11326328-A.

XX PD 26-NOV-1999.

XX PF 13-MAY-1998; 98JP-00130378.

XX PR 13-MAY-1998; 98JP-00130378.

XX PA (MATSU) MATSUMOTO K.

XX WPI; 2000-078337/07.

XX DR P-PSDB; RAY59451.

XX PT Screening a substance which inhibits combination of the X-linked
XX inhibitor of apoptosis protein.

XX PS Disclosure; Page 28-30; 43pp; Japanese.

CC This sequence encodes the human XIAP protein. The invention relates to a
CC method for screening a substance inhibiting the formation of a complex
CC between XIAP and TAB1, in which X-linked inhibitor of apoptosis protein
CC (XIAP), transforming growth factor-beta activated kinase 1 (TAK1) binding
CC protein 1 (TAB1) and a substance to be tested are contacted with each
CC other and then the presence or formation of a complex between XIAP and
CC TAB1 is detected. The substance can be used as a drug for extracellular
CC matrix protein production enhancement, cell growth inhibition, monocyte
CC migration, physiologically active substance induction, immunosuppression,
CC and beta-amyloid protein deposition. A substance inhibiting the formation
CC of a complex between TAB1 and XIAP as well as between XIAP and TGF-beta
CC (Transforming growth factor-beta) type I and/or type II receptor is
CC useful as a drug

XX SQ Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 U; 0 Other;

Query Match 100.0%; Score 198; DB 3; Length 1659;
Best Local Similarity 100.0%; Pred. No. 3.1e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGACGACGGATCTTACTTTTGGACATGGATATCTCAGTTAAACAAGGCGCGCTT 60
DB 874 TATGACGACGGATCTTACTTTTGGACATGGATATCTCAGTTAAACAAGGCGCGCTT 933
QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATATAAGTAAAGTCTTCACTGTGGA 120
DB 934 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATATAAGTAAAGTCTTCACTGTGGA 993
QY 121 GGAGGGCTTAAGTGGAGCCCGAGTGAAGACCTTTGGACACATGCTAAATGGTAT 180
DB 994 GGAGGGCTTAAGTGGAGCCCGAGTGAAGACCTTTGGACACATGCTAAATGGTAT 1053
QY 181 CCAGGGTGCAAAATATCTG 198
DB 1054 CCAGGGTGCAAAATATCTG 1071

RESULT 3

ACAS6455
ID ACAS6455 standard; cDNA; 1659 BP.

XX AC ACAS6455;

XX DT 06-JUN-2003 (first entry)

XX DE Human signalling pathway polynucleotide probe SEQ ID NO 1053.

XX KW Human; probe; ss; array element; Parkinson's disease;
KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

XX OS Homo sapiens.

XX PN US6500938-B1.

XX PD 31-DEC-2002.

XX PF 30-JAN-1998; 98US-00016434.

XX PR 30-JAN-1998; 98US-00016434.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Au-Young J, Seilhamer JJ;

XX WPI; 2003-352189/33.

XX PT Combination of polynucleotide probes, useful as array elements in a
XX microarray for monitoring the expression of a number of target
XX polynucleotides.

XX PS Claim 1; SEQ ID NO 1053; 65pp; English.

CC The invention relates to a combination which, comprises a number of
 CC polynucleotide probes comprising a sequence selected from one of the 1490
 CC sequences mentioned in the specification. The combination is useful as an
 CC array element in a microarray for monitoring the expression of a number
 CC of target polynucleotides. The microarray is particularly useful in the
 CC diagnosis and treatment of cancer and immunopathology and neuropathology.
 CC The microarray is useful in diagnostics and treatment regimens, drug
 CC discovery and development, toxicological and carcinogenicity studies,
 CC forensics and pharmacogenomics. The microarray is also useful for
 CC monitoring progression of diseases and for developing sophisticated
 CC profiles for the effects of currently available therapeutic drugs. The
 CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
 CC and genomic fragments and in research and diagnostic applications. The
 CC array can detect changes in expression in a large number of genes coding
 CC for different signaling pathway populations which can be used to diagnose
 CC various diseases including cancer e.g. adenocarcinoma and leukaemia.
 CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
 CC and Parkinson's disease. The present sequence represents a polynucleotide
 CC probe of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=06500938B1

XX Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 198; DB 7; Length 1659;
 Best Local Similarity 100.0%; Pred. No. 3.1e-54;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAGCAGGATCTTTACTTTTGGGACATGGATATCTACTCAGTTAAACAGGACGCTT 60
 DB 874 TATGAGCAGGATCTTTACTTTTGGGACATGGATATCTACTCAGTTAAACAGGACGCTT 933
 QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCTACTGTGGA 120
 DB 934 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCTACTGTGGA 993
 QY 121 GGAGGCTTAACGATTTGGAGCCAGTGAAGCCCTTGGGACACATGCTTAATGCTAT 180
 DB 994 GGAGGCTTAACGATTTGGAGCCAGTGAAGCCCTTGGGACACATGCTTAATGCTAT 1053
 QY 181 CCAGGCTGCAAAATATCTG 198
 DB 1054 CCAGGCTGCAAAATATCTG 1071

RESULT 4
 AAK99405
 ID AAK99405 standard; DNA; 2404 BP.
 XX AC AAK99405;
 XX 27-JUN-2002 (first entry)

DE DNA of APP related human homologue hCP35211.

XX Neuroprotective; neurotropic; transgenic fly; Alzheimer's disease; Abeta;
 KW amyloid precursor protein; tissue-specific expression control; human APP;
 KW APP pathway modulator; gene therapy; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 692..1528
 FT /*tag= a
 FT /product= "protein of human homologue hCP35211"
 FT /note= "No start codon"

XX WO200226820-A2.

XX 04-APR-2002.

XX 01-OCT-2001; 2001WO-EP011345.

XX 29-SEP-2000; 2000US-0236893P.
 PR 14-JUN-2001; 2001US-0298309P.
 XX (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;
 PI Reinhardt MWM, Zusman S;
 PI WPI; 2002-315796/35.
 DR P-P8DB; AAC0511.

XX New transgenic fly, containing DNA encoding an Abeta portion of human
 APP, useful for identifying agents which modulate the APP pathway and
 PT which can be used to treat Alzheimer's disease.

XX Example 4; Page 111; 129pp; English.

XX The invention relates to a transgenic fly whose genome comprises DNA
 CC encoding a polypeptide having the Abeta portion of human amyloid
 CC precursor protein (APP), fused to a signal sequence. The DNA sequence
 CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
 CC the specification. The DNA sequence is operably linked to a tissue-
 CC specific expression control sequence. Expression of the sequence gives
 CC the fly an altered phenotype. The purpose of the invention is for
 CC identifying agents that inhibit or promote the expression and/or function
 CC of genes or encoded polypeptides which modify the APP pathway. The agent
 CC is a compound, triple helix DNA, antisense oligonucleotide, double
 CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used
 CC to treat conditions such as Alzheimer's disease. The agent can be used as
 CC an APP pathway modulator or in gene therapy. This polynucleotide sequence
 CC represents the DNA of the APP related human homologue hCP35211

XX Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 198; DB 6; Length 2404;
 Best Local Similarity 100.0%; Pred. No. 3.5e-54;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAGCAGGATCTTTACTTTTGGGACATGGATATCTACTCAGTTAAACAGGACGCTT 60
 DB 827 TATGAGCAGGATCTTTACTTTTGGGACATGGATATCTACTCAGTTAAACAGGACGCTT 886
 QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTCTACTGTGGA 120
 DB 887 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTCTACTGTGGA 946
 QY 121 GGAGGCTTAACGATTTGGAGCCAGTGAAGCCCTTGGGACACATGCTTAATGCTAT 180
 DB 947 GGAGGCTTAACGATTTGGAGCCAGTGAAGCCCTTGGGACACATGCTTAATGCTAT 1006
 QY 181 CCAGGCTGCAAAATATCTG 198
 DB 1007 CCAGGCTGCAAAATATCTG 1024

RESULT 5
 AAT70836
 ID AAT70836 standard; cDNA; 2540 BP.
 XX AC AAT70836;
 XX 02-SEP-1997 (first entry)

XX Human apoptosis inhibitor xiap cDNA.

XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; XIAP; HIV;
 KW AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia;
 KW myocardial infarction; stroke; reperfusion injury;
 KW toxin-induced liver disease; gene therapy; diagnosis; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
FH CDS 34..1527
FT /*tag= a
XX WO9706255-A2.
XX 20-FEB-1997.
XX 05-AUG-1996; 96WO-IB001022.
XX 04-AUG-1995; 95US-00511485.
XX 22-DEC-1995; 95US-00576956.
XX (UYOT-) UNIV OTTAWA.

XX Korneluk RG, Mackenzie AE, Baird S, Liston P;
XX WPI; 1997-154262/14.
XX P-PSDB; AAW19581.

XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
XX inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of
XX susceptibility to apoptotic disease.

XX Claim 12; Page 67-68; 21pp; English.

XX Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and hiap-2
XX genes (AA170836-41) respectively code for a new class of mammalian
XX proteins (AAW19581-86) that are inhibitors of apoptosis (IAP). The xiap
XX gene (for X-linked IAP gene) was isolated from a human foetal brain ZapII
XX cDNA library using an X-linked sequence tag site that shows strong
XX homology with the conserved ring zinc finger domain of baculovirus CpiAP
XX and OpiAP genes. The gene was assigned to chromosome Xq25 by FISH. IAP
XX nucleic acids can be used to express IAP polypeptides in cells and
XX animals to inhibit apoptosis, and as primers and probes to identify and
XX isolate additional IAP genes, as well as in methods for treating diseases
XX and disorders involving apoptosis (anti-apoptotic gene therapy)

XX Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 0 U; 1 Other;

Query Match 100.0%; Score 198; DB 2; Length 2540;
Best Local Similarity 100.0%; Pred. No. 3.6e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAAGAGCAGCTT 60
Db 826 TATGAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAAGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 945
QY 121 GGAGGGCTAACTGATTTGGAGCCAGTGAAGCCCTTGGGAACAACATCTAAATGGTAT 180
Db 946 GGAGGGCTAACTGATTTGGAGCCAGTGAAGCCCTTGGGAACAACATCTAAATGGTAT 1005
QY 181 CCAGGGTGCATATCTG 198
Db 1006 CCAGGGTGCATATCTG 1023

RESULT 6
AAAG4901
ID AAA64901 standard; DNA; 2540 BP.
XX AAA64901;
XX 07-NOV-2000 (first entry)
XX Human X-linked inhibitor of apoptosis DNA.
XX X-linked inhibitor of apoptosis; XIAP; hIAP; MIHA; U45880; antisense;

XX antinflammatory; cytostatic; tumour; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
FH CDS 34..1527
FT /*tag= a
FT /product= "X-linked inhibitor of apoptosis"
XX US6087173-A.
XX 11-JUL-2000.
XX 09-SEP-1999; 99US-00392580.
XX 09-SEP-1999; 99US-00392580.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Cowseert LM, Ackermann EJ;
XX WPI; 2000-498201/44.
XX P-PSDB; AAY99985.
XX Antisense compound useful for research reagents, diagnostics, prophylaxis
XX and for treating disorders associated with X-linked inhibitor of
XX apoptosis, modulates expression of X-linked inhibitor of apoptosis.
XX Example 13; Col 43-48; 33pp; English.

XX The present invention relates to antisense oligonucleotides designed to
XX inhibit expression of the human X-linked inhibitor of apoptosis. The
XX present sequence is the X-linked inhibitor of apoptosis DNA. Modified
XX phosphorothioate 2'-methoxyethyl (2'-MOE) oligonucleotides are more
XX effective inhibitors than unmodified oligonucleotides. The
XX oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis
XX expression in cells and tissues in vitro. The oligonucleotides are also
XX useful for treating animals or humans, prone to a disease associated with
XX X-linked inhibitor of apoptosis. The oligonucleotides may also be used
XX prophylactically to prevent infection, inflammation or tumour formation

XX Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;

Query Match 100.0%; Score 198; DB 3; Length 2540;
Best Local Similarity 100.0%; Pred. No. 3.6e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAAGAGCAGCTT 60
Db 826 TATGAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAAGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 945
QY 121 GGAGGGCTAACTGATTTGGAGCCAGTGAAGCCCTTGGGAACAACATCTAAATGGTAT 180
Db 946 GGAGGGCTAACTGATTTGGAGCCAGTGAAGCCCTTGGGAACAACATCTAAATGGTAT 1005
QY 181 CCAGGGTGCATATCTG 198
Db 1006 CCAGGGTGCATATCTG 1023

RESULT 7
ABK93869
ID ABK93869 standard; cDNA; 2540 BP.
XX ABK93869;
XX 26-AUG-2002 (first entry)
XX Human cDNA encoding inhibitor of apoptosis, XIAP #1.

XX Human; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
KW pancreatic cancer; embryonic development; viral pathogenesis;
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
KW lupus erythematosus; herpes virus infection; pox virus infection;
KW adenovirus infection; proliferative disease.
XX
OS Homo sapiens.
XX WO200226968-A2.
PN
XX
PD 04-APR-2002.
XX
PF 27-SEP-2001; 2001WO-CA001379.
XX
PR 28-SEP-2000; 2000US-00672717.
XX
PA (UYOT-) UNIV OTTAWA.
PA (AEGE-) AGERA THERAPEUTICS INC.
XX
PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX
XX WPI: 2002-479562/51.
DR P-PSDB; ABG65663.
XX
XX Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
PT apoptosis in a cell, for treating cancer and other proliferative
PT diseases.
XX
PS Disclosure; Fig 1; 135pp; English.
XX
XX The invention relates to an inhibitor of apoptosis (IAP) antisense
CC nucleic acid (I) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse or
CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC mammal diagnosed with a proliferative disease. The method is useful for
CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a human IAP
CC cDNA sequence
XX
SQ Sequence 2540 BP; 782 A; 415 C; 549 G; 772 T; 0 U; 22 Other;
Query Match 100.0%; Score 198; DB 6; Length 2540;
Best Local Similarity 100.0%; Pred. No. 3.6e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAGCAGCGATCTTTACTTTTGGACATGGATATCTACTCAGTTAACAGGAGCGCTT 60
DB 826 TATGAGCAGCGATCTTTACTTTTGGACATGGATATCTACTCAGTTAACAGGAGCGCTT 885
QY 61 GCAAGAGCTGGATTATATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTCTACTGGA 120
DB 886 GCAAGAGCTGGATTATATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTCTACTGGA 945
QY 121 GGAGGGCTTAACGTATTGGAAGCCAGTGAAGACCCCTTGGGACAAACATGCTAAATGGTAT 180
DB 946 GGAGGGCTTAACGTATTGGAAGCCAGTGAAGACCCCTTGGGACAAACATGCTAAATGGTAT 1005
QY 181 CCAGGGTCAATATCTG 198
DB 1006 CCAGGGTCAATATCTG 1023

RESULT 8
ABV94283
ID ABV94283 standard; cDNA; 2540 BP.
AC ABV94283;
XX
DT 08-JAN-2003 (first entry)
XX
DE Breast carcinoma related nucleotide sequence SEQ ID NO:274.
XX
KW Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;
KW ss.
XX
OS Homo sapiens.
XX WO200246467-A2.
PN
XX
PD 13-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-IB002811.
XX
PR 08-DEC-2000; 2000US-0254090P.
PR 07-DEC-2001; 2001US-00007926.
XX
XX (IPSO-) IPSOGEN.
XX
XX Bertucci F, Houlgatte R, Birnbaum D, Nguyen C, Viens P, Fert V;
XX WPI; 2002-619023/66.
XX
XX Novel polynucleotide library useful in molecular characterization of a
PT carcinoma, comprising a pool of polynucleotide sequences or its
PT subsequences which are either underexpressed or overexpressed in tumor
PT cells.
XX
PS Claim 1; Page 289; 401pp; English.
XX
XX The present invention describes a polynucleotide library (I) useful in
CC the molecular characterization of a carcinoma, comprising a pool of
CC polynucleotides or its subsequences which are either underexpressed or
CC overexpressed in tumor cells, and correspond to any of the
CC polynucleotide sequences chosen from the 468 sequences given in ABV94010
CC to ABV94477. Also described: (1) a polynucleotide array (II) useful for
CC the prognosis or diagnostic of tumour, comprising (I); and (2) detecting
CC (MI) differentially expressed polynucleotide sequences which are
CC correlated with a cancer, involves obtaining a polynucleotide sample from
CC a patient, and reacting the polynucleotide sample obtained with a probe
CC immobilised on a solid support, where the probe comprises any combination
CC of the polynucleotide sequences of (I) or its expression products encoded
CC by polynucleotide sequences of (I), and detecting the reaction product.
CC (I) have cytostatic activities and can be used as anti-tumour agents. (I)
CC is useful in molecular characterisation of a carcinoma. (I) and (II) are
CC useful for the prognosis or diagnostic of tumour, in differentiating a
CC normal cell from a cancer cell, detecting a hormone sensitive tumour
CC cell, differentiating a tumour with lymph nodes from a tumour without
CC lymph nodes, differentiating antracycline-sensitive tumours from
CC antracycline-insensitive tumours, and classifying good and poor prognosis
CC primary breast tumours. (I) is useful for large-scale molecular
CC characterisation of breast cancer that help in prediction, prognosis and
CC cancer treatment, and for detecting differentially expressed genes that
CC correlated with a cancer
XX
SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;
Query Match 100.0%; Score 198; DB 6; Length 2540;
Best Local Similarity 100.0%; Pred. No. 3.6e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAGCAGCGATCTTTACTTTTGGACATGGATATCTACTCAGTTAACAGGAGCGCTT 60
DB 826 TATGAGCAGCGATCTTTACTTTTGGACATGGATATCTACTCAGTTAACAGGAGCGCTT 885

QY 61 GCAAGAGCTGATTTTATGCTTTAGTGAAGGTGATATAAGTAAAGTCTTTCACTGTGGA 120
 DB 886 GCAAGAGCTGATTTTATGCTTTAGTGAAGGTGATATAAGTAAAGTCTTTCACTGTGGA 945
 QY 121 GGAGGCTTAAGTCTGATTTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
 DB 946 GGAGGCTTAAGTCTGATTTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
 QY 181 CCAGGCTGCAAAATATCTG 198
 DB 1006 CCAGGCTGCAAAATATCTG 1023

RESULT 9
 AAL53731
 ID AAL53731 standard; RNA; 2540 BP.
 XX AC AAL53731;
 XX DT 07-FEB-2003 (first entry)
 XX DE X-linked inhibitor of apoptosis protein 95Q ID No 25.
 XX KW Target RNA; target RNA; support-attached test compound; flow cytometry;
 XX KW mass spectrometry; high-throughput screening; RNA motif; ss.
 XX OS Homo sapiens.
 XX WO200283837-A1.
 XX PD 24-OCT-2002.
 XX PF 11-APR-2002; 2002WO-US011758.
 XX PR 11-APR-2001; 2001US-0282966P.
 XX PA (PTCT-) PTC THERAPEUTICS INC.
 XX PI Alnstead NG;
 XX DR WPI; 2003-075534/07.
 XX PT Identifying a test compound that binds to a target RNA molecule by
 PT separating the detectably labeled target RNA; support-attached test
 PT compound complex from uncomplexed target RNA molecules and test compounds
 PT by flow cytometry.
 XX PS Example; Page 79-80; 131pp; English.
 XX CC The invention relates to a novel method for identifying a test compound
 CC that binds to a target RNA molecule comprising separating the detectably
 CC labeled target RNA; support-attached test compound complex from
 CC uncomplexed target RNA molecules and test compounds. The separating
 CC process is carried out by flow cytometry and determining a structure of
 CC the type of test compound of the RNA; support-attached test compound
 CC complex by mass spectrometry. The method is useful for high-throughput
 CC screening of libraries of compounds to identify pharmaceutical leads.
 CC This polynucleotide sequence represents one of the target RNA motifs/
 CC regions of the invention
 XX SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;
 Query Match 100.0%; Score 198; DB 7; Length 2540;
 Best Local Similarity 100.0%; Pred. No. 3.6e-54;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TATGAACAGCAGATCTTTACTTTTGGACATGATATCTAGTTAAACAGAGCAGCTT 60
 DB 826 TATGAACAGCAGATCTTTACTTTTGGACATGATATCTAGTTAAACAGAGCAGCTT 885
 QY 61 GCAAGAGCTGATTTTATGCTTTAGTGAAGGTGATATAAGTAAAGTCTTTCACTGTGGA 120
 DB 886 GCAAGAGCTGATTTTATGCTTTAGTGAAGGTGATATAAGTAAAGTCTTTCACTGTGGA 945

QY 121 GGAGGCTTAAGTCTGATTTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
 DB 946 GGAGGCTTAAGTCTGATTTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
 QY 181 CCAGGCTGCAAAATATCTG 198
 DB 1006 CCAGGCTGCAAAATATCTG 1023

RESULT 10
 AAD49663
 ID AAD49663 standard; DNA; 2540 BP.
 XX AC AAD49663;
 XX DT 24-MAR-2003 (first entry)
 XX DE Human X-linked inhibitor of apoptosis protein (XIAP) DNA.
 XX KW Amyloidosis; haemophilia; Alzheimer's disease; atherosclerosis; cancer;
 KW gigantism; dwarfism; hypothyroidism; hyperthyroidism; cystic fibrosis;
 KW autoimmune disorder; aging; inflammation; diabetes; obesity; anorectic;
 KW neurodegenerative disorder; Parkinson's disease; gene therapy; viricide;
 KW haemostatic; antibacterial; nootropic; neuroprotective; cytostatic; XIAP;
 KW fungicide; human; X-linked inhibitor of apoptosis protein; gene; ds.
 XX OS Homo sapiens.
 XX WO200283953-A1.
 XX PD 24-OCT-2002.
 XX PF 11-APR-2002; 2002WO-US011757.
 XX PR 11-APR-2001; 2001US-0282965P.
 XX PA (PTCT-) PTC THERAPEUTICS INC.
 XX PI Rando R, Welch B;
 XX DR WPI; 2003-075561/07.
 XX PT Identifying a test compound that binds to a target RNA molecule for
 PT treating or preventing amyloidosis, hemophilia, cancer, gigantism,
 PT diabetes, by contacting a detectably labeled target RNA molecule with a
 PT library of test compounds.
 XX PS Example; Page 88-89; 152pp; English.
 XX CC The invention relates to a method for identifying a test compound that
 CC binds to a target RNA molecule, which comprises contacting a detectably
 CC labelled target RNA molecule with a library of test compounds under
 CC conditions that permit direct binding of the labelled target RNA to a
 CC member of the library of test compounds so that a detectably labeled
 CC target RNA: test compound complex is formed. The method is useful for
 CC screening libraries of compounds for those that are selectively bind to a
 CC pre-selected target RNA. The compounds are useful for inhibiting the
 CC formation of a specific bound RNA: host cell factor complexes in vivo.
 CC They are also useful for treating or preventing diseases associated with
 CC overproduction or decreased protein function, such as amyloidosis,
 CC haemophilia, Alzheimer's disease, atherosclerosis, cancer, gigantism,
 CC dwarfism, hypothyroidism, hyperthyroidism, autoimmune disorders, aging,
 CC inflammation, cystic fibrosis, diabetes, obesity, neurodegenerative
 CC disorders, Parkinson's disease or infections (bacterial, viral, fungal).
 CC The invention is also used in gene therapy. The present sequence is human
 CC X-linked inhibitor of apoptosis protein (XIAP) DNA. This sequence is used
 CC to illustrate the method of the invention
 XX SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;
 Query Match 100.0%; Score 198; DB 7; Length 2540;
 Best Local Similarity 100.0%; Pred. No. 3.6e-54;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCAGGATCTTTTACTTTGGGACATGATATACAGTTAAACAGGACGCTT 60
DB 826 TATGAAGCAGGATCTTTTACTTTGGGACATGATATACAGTTAAACAGGACGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGTGATAAAGTAAAGTCTTTCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGTGATAAAGTAAAGTCTTTCACTGTGGA 945
QY 121 GGAGGGCTAACTGATTTGAGGAGCCAGTGAAGACCTTGGGAACACATGCTAAATGGTAT 180
DB 946 GGAGGGCTAACTGATTTGAGGAGCCAGTGAAGACCTTGGGAACACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAAAATATCTG 198
DB 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 11
ADB81002
ID ADB81002 standard; DNA; 2540 BP.
AC ADB81002;
XX
DT
DT
XX
XX
DE
XX
KW RING-SH 3; Gag protein; Gag late domain; PI3K; actin; myosin; Hsp60;
KW Hsp70; Hsp90; STAM1; STAM2A; STAM2B; VHS-UIM; GTPase; E2 enzyme; teg101;
KW cullin; RING-SH; Clathrin; virucide; vaccine; antiviral; retrovirus;
KW rhadovirus; filovirus; gene; ds.
XX
OS Unidentified.
PN WO2003033646-A2.
XX
XX
PD 24-APR-2003.
XX
PF 31-JUL-2002; 2002WO-US024589.
XX
PR 31-JUL-2001; 2001US-0308958P.
PR 09-NOV-2001; 2001US-0345846P.
XX
XX (PROT-) PROTEOLOGICS INC.
XX
XX Greener T, Moskowitz H, Reiss Y, Alroy I;
XX WPI; 2003-393509/37.
XX P-PSDB; ADB80961.
XX

New isolated protein complex comprising a RING-SH 3 polypeptide and another polypeptide, useful for detecting cells infected with a virus, and for treating viral disorders caused by retroviruses, rhadoviruses, or filoviruses.
XX
XX Disclosure; Fig 75; 176pp; English.
XX
XX The invention relates to a novel isolated protein complex comprising a RING-SH 3 polypeptide and a polypeptide selected from a Gag protein, a Gag late domain, PI3K, actin, myosin, Hsp60, Hsp70, Hsp90, STAM1, STAM2A, STAM2B, VHS-UIM, a GTPase, an E2 enzyme, teg101, a cullin, RING-SH, and a clathrin. The novel protein complex has virucide activity and can be used to treat disorders as part of a vaccine. The protein complex and composition are useful for detecting cells infected with a virus, for identifying agents having antiviral activity, and for treating viral disorders caused by retroviruses, rhadoviruses, or filoviruses. This polynucleotide represents a DNA sequence relating to a protein comprising the RING-SH complex of the invention.
XX
XX Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;

Query Match 100.0%; Score 198; DB 8; Length 2540;
Best Local Similarity 100.0%; Pred. No. 3.6e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCAGGATCTTTTACTTTGGGACATGATATACAGTTAAACAGGACGCTT 60
DB 826 TATGAAGCAGGATCTTTTACTTTGGGACATGATATACAGTTAAACAGGACGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGTGATAAAGTAAAGTCTTTCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGTGATAAAGTAAAGTCTTTCACTGTGGA 945
QY 121 GGAGGGCTAACTGATTTGAGGAGCCAGTGAAGACCTTGGGAACACATGCTAAATGGTAT 180
DB 946 GGAGGGCTAACTGATTTGAGGAGCCAGTGAAGACCTTGGGAACACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAAAATATCTG 198
DB 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 12
ABK93875
ID ABK93875 standard; cDNA; 3000 BP.
XX
AC ABK93875;
XX
DT 26-AUG-2002 (first entry)
XX
DE Human cDNA encoding inhibitor of apoptosis, XIAP #2.
XX
KW Human; es; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
KW pancreatic cancer; embryonic development; viral pathogenesis;
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
KW lupus erythematosus; herpes virus infection; pox virus infection;
KW adenovirus infection; proliferative disease.
XX
OS Homo sapiens.
XX
XX WO200226968-A2.
XX
XX 04-APR-2002.
XX
XX 27-SEP-2001; 2001WO-CA001379.
XX
XX 28-SEP-2000; 2000US-00672717.
XX
XX (UYOT-) UNIV OTTAWA.
XX (AEGE-) AEGERA THERAPEUTICS INC.
XX
XX Korneiluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX WPI; 2002-479562/51.
XX
XX Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing apoptosis in a cell, for treating cancer and other proliferative diseases.
XX
XX Example 2; Fig 15; 135pp; English.
XX
XX The invention relates to an inhibitor of apoptosis (IAP) antisense nucleic acid (I) that inhibits IAP biological activity, regardless of length of the antisense nucleic acid, the IAP proteins may be mouse or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical composition comprising a mammalian IAP antisense molecule and a method of enhancing apoptosis in a cell, comprising administering a negative regulator of the IAP anti-apoptotic pathway to the cell. The IAP antisense inhibitor is useful for enhancing apoptosis in a cell in a mammal diagnosed with a proliferative disease. The method is useful for treating a patient diagnosed with a proliferative disease like cancer. The IAP antisense molecule is useful to treat, ameliorate, improve, sustain or prevent proliferative diseases (e.g. ovarian cancer, CC

CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a human IAP
 CC cDNA sequence

XX Sequence 3000 BP; 974 A; 452 C; 601 G; 973 T; 0 U; 0 Other;

Query Match 100.0%; Score 198; DB 6; Length 3000;

Best Local Similarity 100.0%; Pred. No. 3.8e-54;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGATCTTTACTTTTGGGACATGGATATCACTCAGTTAACAGAGCAGCTT 60

DB 1482 TATGAGCAGCGATCTTTACTTTTGGGACATGGATATCACTCAGTTAACAGAGCAGCTT 1541

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCACTGTGGA 120

DB 1542 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCACTGTGGA 1601

QY 121 GGAGGCTAACTGATTGGAAGCCAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 180

DB 1602 GGAGGCTAACTGATTGGAAGCCAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 1661

QY 181 CCAGGCTGCAATATCTG 198

DB 1662 CCAGGCTGCAATATCTG 1679

RESULT 13

AAV55038

ID AAV55038 standard; cDNA; 5232 BP.

XX

AC AAV55038;

XX

DT 13-NOV-1998 (first entry)

XX

DE Human XIAP coding sequence.

XX

XX Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;

KW proliferative disease; IAP; therapy; cancer; human; XIAP protein; ss.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT 34..1527

FT /*tag= a

FT /product= "XIAP"

XX

XX WO9835693-A2.

XX

XX 20-AUG-1998.

XX

XX 13-FEB-1998; 98WO-IB000781.

XX

XX 13-FEB-1997; 97US-00800929.

XX

XX (UYOT-) UNIV OTTAWA.

XX

XX Korneluk R, Mackenzie AE, Liston P, Baird S, Tsang B, Pratt C;

XX WPI; 1998-467164/40.

XX P-PSDB; AAW69294.

XX

XX Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP

FT or NAIP polypeptide - also methods for prognosis based on presence of IAP

FT and NAIP, specifically applied to cancers involving p53 mutations.

XX

XX Claim 13; Fig 1; 147pp; English.

XX

XX This sequence encodes the human XIAP protein, which is an inhibitor of

CC apoptosis protein (IAP), and can be used in the method of the invention.

XX

CC The method is for enhancing apoptosis in cells from a mammal with
 CC proliferative disease by treatment with a compound that inhibits
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory
 CC compounds are used to treat proliferative diseases, specially cancers of
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
 CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,
 CC rectum, cervix or endometrium, particularly to increase their sensitivity
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
 CC detected in many cancers and are associated with poor prognosis,
 CC resistance to chemotherapeutic agents and mutations in p53 (it is
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
 CC genes). Transgenic animals are used for testing the effects of antisense
 CC oligonucleotides and for screening for the inhibitors

XX Sequence 5232 BP; 1579 A; 861 C; 1062 G; 1728 T; 0 U; 2 Other;

Query Match 100.0%; Score 198; DB 2; Length 5232;

Best Local Similarity 100.0%; Pred. No. 4.6e-54;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGATCTTTACTTTTGGGACATGGATATCACTCAGTTAACAGAGCAGCTT 60

DB 826 TATGAGCAGCGATCTTTACTTTTGGGACATGGATATCACTCAGTTAACAGAGCAGCTT 385

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCACTGTGGA 120

DB 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCACTGTGGA 945

QY 121 GGAGGCTAACTGATTGGAAGCCAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 180

DB 946 GGAGGCTAACTGATTGGAAGCCAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGCTGCAATATCTG 198

DB 1006 CCAGGCTGCAATATCTG 1023

RESULT 14

AAO03575

ID AAO03575 standard; cDNA; 1752 BP.

XX

AC AAO03575;

XX

DT 19-JUN-2001 (first entry)

XX

XX Human IAP-like protein-3 (ILP-3) cDNA.

XX

XX Human; inhibitor of apoptosis; IAP-like protein-3; ILP-3;

XX chromosome 2q12-q14; transforming growth factor beta receptor; TGFbetaR;

XX c-Jun N-terminal kinase; JNK; gene therapy; osteoarthritis; cytostatic;

XX hypothyroidism; juvenile nephronophthisis; thrombophilia; cancer;

XX colorectal cancer; neonatal purpura fulminans; autoimmune disease;

XX diabetes; multiple sclerosis; neurodegenerative disease;

XX retinal degeneration; ss.

XX

XX Homo sapiens.

XX

XX Key Location/Qualifiers

FT 847..1197

FT /*tag= a

FT /product= "Human inhibitor of apoptosis (IAP)-like

FT protein-3 (hILP-3);"

XX

XX WO200123568-A2.

XX

XX 05-APR-2001.

XX

XX 29-SEP-2000; 2000WO-US026735.

XX

XX 30-SEP-1999; 99US-0157169P.

XX

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

```
PI Duckett C, Mir SS;
XX WPI; 2001-258135/26.
DR P-PSDB; AAE00359.
XX
XX Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with
PT transforming growth factor beta receptor modulating activity, and the
PT nucleic acids that encode them, useful for treating, e.g. diabetes and
XX multiple sclerosis.
XX
XX Claim 18; Page 87-88; 108pp; English.
PS
PS
CC The present sequence is human inhibitor of apoptosis (IAP)-like protein-3
CC (ILP-3) cDNA. The ILP-3 gene is located on chromosome 2q12-q14. ILP-3
CC comprises a spacer region and a ring finger domain. The IAP interacts
CC with transforming growth factor beta receptor (TGFbetaR) and modulates
CC TGFbetaR activity. ILP-3 also moderately inhibits ILP-1 mediated c-Jun N-
CC terminal kinase (JNK) activation when co-transfected with ILP-1. Such
CC activity decreases or prevents apoptosis in a cell. ILP-3 is used in the
CC area of genetic testing for predisposition to diseases, such as
CC osteoarthritis, hypothyroidism, juvenile nephronophthisis, thrombophilia,
CC colorectal cancer and neonatal purpura fulminans owing to an ILP-3
CC deletion or mutation. The ILP is also used in the treatment of diseases
CC associated with abnormal apoptosis such as cancer, autoimmune diseases,
CC e.g., diabetes and multiple sclerosis and neurodegenerative diseases
CC including retinal degeneration. The ILP-3 gene is also used in gene
CC therapy for treating patients suffering from ILP-3 gene deletions or
CC mutations
XX
XX SQ Sequence 1752 BP; 530 A; 299 C; 385 G; 538 T; 0 U; 0 Other;
Query Match 91.1%; Score 180.4; DB 4; Length 1752;
Best Local Similarity 94.4%; Pred. No. 1.8e-48;
Matches 187; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 1 TATGAGCAGCGATCTTTACTTTTGGGACATGATATCTAGTTAACAGGACGCTT 60
DB 499 TATGAGCAGCGATCTTTACTTTTGGGATGTGGATATATTCAGTTAACAGGACGCTT 558
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA 120
DB 559 TCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA 618
QY 121 GGAGGGCTAACTGATTGGAGCCCGAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
DB 619 GGGGGGCTAACTGATTGGAGCCCGAGTGAAGACCCCTTGGGAACAACATGATAAATGGCAT 678
QY 181 CCAGGGTGCAAAATATCTG 198
DB 679 CCAGGGTGCAAAATATCTG 696
RESULT 15
AAAT7210
ID AAAT7210 standard; DNA; 1988 BP.
XX
XX AC AAAT7210;
XX
XX 16-SEP-1997 (first entry)
XX
XX Mouse inhibitor of apoptosis protein homologue MIHA DNA.
XX
XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA;
KW degenerative disease; infectious disease; autoimmune disease; cancer;
KW gene therapy; diagnosis; ss.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX CDS 212..1702
XX /*cag= a
XX
XX W09723501-A1.
```

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XX 03-JUL-1997.
XX
XX 20-DEC-1996; 96WO-AU000827.
XX
XX 22-DEC-1995; 95AU-00007275.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Vaux DL;
XX
XX WPI; 1997-350966/32.
XX
XX P-PSDB; AAW19745.
XX
XX Isolated protein homologues of viral inhibitors of apoptosis - used to
XX modulate apoptosis for treatment of degenerative, infectious or
XX autoimmune diseases and cancer.
XX
XX Claim 24; Page 44-47; 136pp; English.
XX
XX An isolated nucleic acid molecule (AAAT72710) codes for mammalian IAP
XX homologue A (MIHA) (AAW19745), a murine homologue of baculovirus
XX inhibitor of apoptosis protein (IAP). It was isolated from a mouse liver
XX cDNA library on the basis of homology to Orfgyia pseudotsugata
XX polyhedrosis virus IAP BIR and RING finger amino acid motifs. Animal IAP
XX homologue nucleic acids (see also AAAT72711-17) can be used to produce
XX polypeptides useful in methods for modulating apoptosis in animal cells,
XX specifically for treatment, by inhibition, of degenerative and infectious
XX disease or, by promotion, of cancer and autoimmune disease, and can be
XX used for gene therapy of these diseases
XX
XX SQ Sequence 1988 BP; 605 A; 367 C; 459 G; 557 T; 0 U; 0 Other;
Query Match 88.2%; Score 174.6; DB 2; Length 1988;
Best Local Similarity 92.9%; Pred. No. 1.4e-46;
Matches 193; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1 TATGAGCAGCGATCTTTACTTTTGGGACATGATATCTAGTTAACAGGACGCTT 60
DB 1001 TATGAGCAGCGATCTTTACTTTTGGAAACATGGACATCTCTCAGTTAACAGGACGCTT 1060
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA 120
DB 1061 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA 1120
QY 121 GGAGGGCTAACTGATTGGAGCCCGAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
DB 1121 GGAGGGCTCAGCGATTGGAGCCCGAGTGAAGACCCCTTGGGAACAACATGCGAAGTGGTAC 1180
QY 181 CCAGGGTGCAAAATATCT 197
DB 1181 CCAGGGTGCAAAATATCT 1197
Search completed: March 13, 2004, 04:35:13
Job time : 270 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 13, 2004, 04:07:08 ; Search time 62 Seconds
(without alignments)
1772.263 Million cell updates/sec

Title: US-09-654-743-47

Perfect score: 198
Sequence: 1 tatgaagcaggtattttac.....atccagggtgcaaatatctg 198

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTCUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	100.0	1588	4	US-09-239-867-3
2	198	100.0	1659	4	US-09-016-434-1053
3	198	100.0	2540	2	US-08-511-485-5
4	198	100.0	2540	3	US-09-392-580-1
5	198	100.0	2540	4	US-09-201-936-3
6	198	100.0	2540	4	US-09-023-655-900
7	198	100.0	2540	4	US-09-011-356-3
8	198	100.0	2540	4	US-09-672-717-218
9	198	100.0	3000	4	US-09-672-717-231
10	198	100.0	5232	3	US-09-212-971-3
11	198	100.0	5232	3	US-08-800-929A-3
12	198	100.0	5232	4	US-09-617-053A-9
13	173	87.4	2100	2	US-08-511-485-9
14	173	87.4	2100	4	US-09-201-936-9
15	173	87.4	2100	4	US-09-011-356-9
16	173	87.4	2100	4	US-09-672-717-224
17	169.8	85.8	2691	3	US-09-212-971-9
18	169.8	85.8	2691	3	US-08-800-929A-9
19	169.8	85.8	2691	4	US-09-617-053A-9
20	164.4	83.0	711	3	US-09-121-979-3
21	164.4	83.0	711	3	US-09-332-319-3
22	164.4	83.0	1559	4	US-09-239-867-1
23	157.8	79.7	152331	3	US-09-128-155-16
24	131.4	66.4	176373	3	US-09-128-155-17
25	78.6	39.7	2563	4	US-09-016-434-1076
26	78.6	39.7	2563	4	US-09-023-655-894
27	78.6	39.7	2601	3	US-08-569-749-3

28	78.6	39.7	2601	5	PCT-US96-12860-3	Sequence 3, Appli
29	78.6	39.7	2676	2	US-08-511-485-5	Sequence 5, Appli
30	78.6	39.7	2676	4	US-09-201-936-5	Sequence 5, Appli
31	78.6	39.7	2676	4	US-09-011-356-5	Sequence 5, Appli
32	78.6	39.7	2676	4	US-09-672-717-220	Sequence 220, App
33	78.6	39.7	3076	2	US-09-205-144-1	Sequence 1, Appli
34	78.6	39.7	6669	3	US-09-212-971-5	Sequence 5, Appli
35	78.6	39.7	6669	3	US-08-800-929A-5	Sequence 5, Appli
36	78.6	39.7	6669	4	US-09-617-053A-5	Sequence 5, Appli
37	78.6	39.7	6669	4	US-09-672-717-230	Sequence 230, App
38	74.4	37.6	1435	5	PCT-US95-05922A-1	Sequence 1, Appli
39	74.4	37.6	2580	2	US-08-511-485-7	Sequence 7, Appli
40	74.4	37.6	2580	4	US-09-011-356-7	Sequence 7, Appli
41	74.4	37.6	2580	4	US-09-672-717-222	Sequence 222, App
42	74.4	37.6	2589	3	US-08-569-749-1	Sequence 1, Appli
43	74.4	37.6	2589	3	PCT-US96-12860-1	Sequence 1, Appli
44	74.4	37.6	2589	5	PCT-US96-12860-1	Sequence 1, Appli
45	74.4	37.6	3532	2	US-09-205-204-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-239-867-3
; Sequence 3, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-239-867-3

Query Match	100.0%	Score 198;	DB 4;	Length 1588;
Best Local Similarity	100.0%	Pred. No. 1.5e-59;		
Matches 198;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTACTCAGTTAACAGGAGCAGCTT	60	
DB	826	TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTACTCAGTTAACAGGAGCAGCTT	885	
QY	61	GCAAGAGCTGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGA	120	
DB	886	GCAAGAGCTGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGA	945	
QY	121	GGAGGGCTTAAGTATGGAGCCAGTGAAGCCCTTGGGACCAACATGCTTAATGCTAT	180	
DB	946	GGAGGGCTTAAGTATGGAGCCAGTGAAGCCCTTGGGACCAACATGCTTAATGCTAT	1005	
QY	181	CCAGGGTGCATATATCTG 198		
DB	1006	CCAGGGTGCATATATCTG 1023		

RESULT 2
US-09-016-434-1053
; Sequence 1053, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1053:
SEQUENCE CHARACTERISTICS:
LENGTH: 1659 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENEBANK
CLONE: G1016687
US-09-016-434-1053

Query Match 100.0%; Score 198; DB 4; Length 1659;
Best Local Similarity 100.0%; Pred. No. 1.5e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCAGGATCTTTACTTTGGGACATGATATCTAGTAAACAAGGAGCAGCTT 60
DB 874 TATGAAGCAGGATCTTTACTTTGGGACATGATATCTAGTAAACAAGGAGCAGCTT 933
QY 61 GCAGAGCTGGATTTTATGCTTTAGTGAAGGTGATAAGTAAAGTCTTCACTGTGGA 120
DB 934 GCAGAGCTGGATTTTATGCTTTAGTGAAGGTGATAAGTAAAGTCTTCACTGTGGA 993
QY 121 GGAGGGCTAACTGATTTGGAGCCCTGGAAGCCCTTGGGAAACAACATGCTAAATGGTAT 180
DB 994 GGAGGGCTAACTGATTTGGAGCCCTGGAAGCCCTTGGGAAACAACATGCTAAATGGTAT 1053
QY 181 CCAGGGTGCAAAATATCTG 198
DB 1054 CCAGGGTGCAAAATATCTG 1071

RESULT 3
US-08-511-485-3
Sequence 3, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2540 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)
US-08-511-485-3

Query Match 100.0%; Score 198; DB 2; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1.8e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCAGGATCTTTACTTTGGGACATGATATCTAGTAAACAAGGAGCAGCTT 60
DB 826 TATGAAGCAGGATCTTTACTTTGGGACATGATATCTAGTAAACAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGAAGGTGATAAGTAAAGTCTTCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTTATGCTTTAGTGAAGGTGATAAGTAAAGTCTTCACTGTGGA 945
QY 121 GGAGGGCTAACTGATTTGGAGCCCTGGAAGCCCTTGGGAAACAACATGCTAAATGGTAT 180
DB 946 GGAGGGCTAACTGATTTGGAGCCCTGGAAGCCCTTGGGAAACAACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAAAATATCTG 198
DB 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 4
US-09-392-580-1
Sequence 1, Application US/09392580
Patent No. 6087173
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRE
FILE REFERENCE: RTS-0072
CURRENT APPLICATION NUMBER: US/09/392,580
CURRENT FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
LENGTH: 2540
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (34)..(1527)

US-09-392-580-1

Query Match 100.0%; Score 198; DB 3; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1.8e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTTACCTTTTGGGACATGGATATCTCAGTTAAAGGAGCAGCTT 60
DB 826 TATGAAGCAGCGATCTTTTACCTTTTGGGACATGGATATCTCAGTTAAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGTGATAAAGTAAAGTCTTTCACCTGTGGA 120
DB 886 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGTGATAAAGTAAAGTCTTTCACCTGTGGA 945
QY 121 GGAGGCTAACTGATTGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
DB 946 GGAGGCTAACTGATTGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAAAATATCTG 198
DB 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 5

US-09-201-936-3
; Sequence 3, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/TB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)...(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-3

Query Match 100.0%; Score 198; DB 4; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1.8e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTTACCTTTTGGGACATGGATATCTCAGTTAAAGGAGCAGCTT 60
DB 826 TATGAAGCAGCGATCTTTTACCTTTTGGGACATGGATATCTCAGTTAAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGTGATAAAGTAAAGTCTTTCACCTGTGGA 120
DB 886 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGTGATAAAGTAAAGTCTTTCACCTGTGGA 945
QY 121 GGAGGCTAACTGATTGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
DB 946 GGAGGCTAACTGATTGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAAAATATCTG 198
DB 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 6

US-09-023-655-900
; Sequence 900, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Sellhammer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 900:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2540 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1184319
US-09-023-655-900

Query Match 100.0%; Score 198; DB 4; Length 2540;

Best Local Similarity 100.0%; Pred. No. 1.8e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTTACCTTTTGGGACATGGATATCTCAGTTAAAGGAGCAGCTT 60
DB 826 TATGAAGCAGCGATCTTTTACCTTTTGGGACATGGATATCTCAGTTAAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGTGATAAAGTAAAGTCTTTCACCTGTGGA 120
DB 886 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGTGATAAAGTAAAGTCTTTCACCTGTGGA 945
QY 121 GGAGGCTAACTGATTGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
DB 946 GGAGGCTAACTGATTGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAAAATATCTG 198
DB 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 7
US-09-011-356-3
; Sequence 3, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Lison, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; CURRENT FILING DATE: 1998-09-14
; EARLIER FILING DATE: 1996-01-022
; EARLIER FILING DATE: 1996-08-05
; EARLIER FILING DATE: 1995-12-22
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: variation
; LOCATION: (2540)...(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-011-356-3

Query Match 100.0%; Score 198; DB 4; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1.8e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 60
DB 826 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGGTGATATAAGTAAAGTCTTTCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTATGCTTTAGTGAAGGTGATATAAGTAAAGTCTTTCACTGTGGA 945
QY 121 GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACACATGCTAAATGGTAT 180
DB 946 GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAAAATATCTG 198
DB 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 8
US-09-672-717-218
; Sequence 218, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; FILE REFERENCE: 07891/025001
; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 218

; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)...(2540)
; OTHER INFORMATION: n=a,t,c, or g
US-09-672-717-218
Query Match 100.0%; Score 198; DB 4; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1.8e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 60
DB 826 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGGTGATATAAGTAAAGTCTTTCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTATGCTTTAGTGAAGGTGATATAAGTAAAGTCTTTCACTGTGGA 945
QY 121 GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACACATGCTAAATGGTAT 180
DB 946 GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAAAATATCTG 198
DB 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 9
US-09-672-717-231
; Sequence 231, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; FILE REFERENCE: 07891/025001
; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 3000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-672-717-231

Query Match 100.0%; Score 198; DB 4; Length 3000;
Best Local Similarity 100.0%; Pred. No. 2e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 60
DB 1482 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 1541
QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGGTGATATAAGTAAAGTCTTTCACTGTGGA 120
DB 1542 GCAAGAGCTGGATTTATGCTTTAGTGAAGGTGATATAAGTAAAGTCTTTCACTGTGGA 1601
QY 121 GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACACATGCTAAATGGTAT 180
DB 1602 GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACACATGCTAAATGGTAT 1661
QY 181 CCAGGGTGCAAAATATCTG 198
DB 1662 CCAGGGTGCAAAATATCTG 1679

RESULT 12
US-09-617-053A-3
; Sequence 3, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Kortheluk, Robert G
; APPLICANT: Mackenzie, Alexander E

APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 5232
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (4623)...(4623)
OTHER INFORMATION: n can be any nucleotide
NAME/KEY: variation
LOCATION: (4622)...(4622)
OTHER INFORMATION: n can be any nucleotide
US-09-617-053A-3

Query Match 100.0%; Score 198; DB 4; Length 5232;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTTACTTTTGGACATGGATATCTCAGTTAACAGGACGCTT 60
DB 826 TATGAAGCAGGATCTTTACTTTTGGACATGGATATCTCAGTTAACAGGACGCTT 885

QY 61 GCAAGAGCTGGATTTTATCTTTAGTGAAGTGATAAAGTAAAGTCTTTCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTTATCTTTAGTGAAGTGATAAAGTAAAGTCTTTCACTGTGGA 945

QY 121 GGAGGGCTAACTGATGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
DB 946 GGAGGGCTAACTGATGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAATATCTG 198
DB 1006 CCAGGGTGCAATATCTG 1023

RESULT 13
US-08-511-485-9
Sequence 9, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485

FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2100 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)
US-08-511-485-9

Query Match 87.4%; Score 173; DB 2; Length 2100;
Best Local Similarity 92.4%; Pred. No. 9.6e-51;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTTACTTTTGGACATGGATATCTCAGTTAACAGGACGCTT 60
DB 916 TATGAAGCAGGATCTTTACTTTTGGACATGGATATCTCAGTTAACAGGACGCTT 975

QY 61 GCAAGAGCTGGATTTTATCTTTAGTGAAGTGATAAAGTAAAGTCTTTCACTGTGGA 120
DB 976 GCAAGAGCTGGATTTTATCTTTAGTGAAGTGATAAAGTAAAGTCTTTCACTGTGGA 1035

QY 121 GGAGGGCTAACTGATGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
DB 1036 GGAGGGCTAACTGATGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1095

QY 181 CCAGGGTGCAATATCT 197
DB 1096 CCAGGGTGCAATATCT 1112

RESULT 14
US-09-201-936-9
Sequence 9, Application US/09201936
Patent No. 6541457
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FASCTSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 2100
TYPE: DNA
ORGANISM: Mus musculus
US-09-201-936-9

Query Match 87.4%; Score 173; DB 4; Length 2100;
Best Local Similarity 92.4%; Pred. No. 9.6e-51;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Db |||||||
QY 916 TATGAAGCAGGATCGTTACTTTTGGACATGGATATACCTACGTTAAACAGGAGCAGCTT 975
Db |||||||
QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTGCCTTTCACTGTGGA 120
Db |||||||
QY 976 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTGCCTTTCACTGTGGA 1035
Db |||||||
QY 121 GGAGGGCTAACTGATTTGAAGCCAGTGAAGCCCTTGGGAACAACATGCTAAATGCTAT 180
Db |||||||
QY 1036 GGAGGGCTCAGCGATTGAAGCCAAAGTGAAGCCCTTGGGACCAGCATGCTAAGTCTAC 1095
Db |||||||
QY 181 CCAGGGTGCAAAATATCT 197
Db |||||||
QY 1096 CCAGGGTGCAAAATACCT 1112
Db |||||||
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RESULT 15

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US-09-011-356-9
; Sequence 9, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011.356A
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-011-356-9
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Query Match 87.4%; Score 173; DB 4; Length 2100;
Best Local Similarity 92.4%; Pred. No. 9.6e-51;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
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QY 1 TATGAAGCAGGATCTTTTACTTTTGGACATGGATATACCTACGTTAAACAGGAGCAGCTT 60
Db |||||||
QY 916 TATGAAGCAGGATCGTTACTTTTGGACATGGATATACCTACGTTAAACAGGAGCAGCTT 975
Db |||||||
QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTGCCTTTCACTGTGGA 120
Db |||||||
QY 976 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTGCCTTTCACTGTGGA 1035
Db |||||||
QY 121 GGAGGGCTAACTGATTTGAAGCCAGTGAAGCCCTTGGGAACAACATGCTAAATGCTAT 180
Db |||||||
QY 1036 GGAGGGCTCAGCGATTGAAGCCAAAGTGAAGCCCTTGGGACCAGCATGCTAAGTCTAC 1095
Db |||||||
QY 181 CCAGGGTGCAAAATATCT 197
Db |||||||
QY 1096 CCAGGGTGCAAAATACCT 1112
Db |||||||
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Search completed: March 13, 2004, 06:26:51
Job time : 64 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 13, 2004, 04:27:28 ; Search time 207 Seconds

(without alignments)
3521.528 Million cell updates/sec

Title: US-09-654-743-47

Perfect score: 198

Sequence: 1 tatgaacagcgatctttac.....atccagggtgcaaatatctg 198

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2432557 seqs, 184079884 residues

Total number of hits satisfying chosen parameters: 4865114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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- 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198	100.0	1659	15	US-10-305-720-1053
2	198	100.0	2404	9	US-09-964-899-38
3	198	100.0	2540	9	US-09-201-936-3
4	198	100.0	2540	14	US-10-007-926A-274
5	198	100.0	5232	9	US-09-974-592-3
6	173	87.4	2100	9	US-09-201-936-9
7	169.8	85.8	2691	9	US-09-974-592-9
8	157.8	79.7	152331	13	US-10-095-407-16
9	131.4	66.4	176373	13	US-10-095-407-17
10	78.6	39.7	255	14	US-10-102-524-906
11	78.6	39.7	2563	15	US-10-305-720-1076
12	78.6	39.7	2601	14	US-10-232-286-3
13	78.6	39.7	2676	9	US-09-201-936-5
14	78.6	39.7	2916	12	US-10-240-425-1436
15	78.6	39.7	3076	9	US-09-954-456-1635

16	78.6	39.7	3076	9	US-09-954-531-16	Sequence 16, Appli
17	78.6	39.7	3076	14	US-10-197-290-1	Sequence 1, Appli
18	78.6	39.7	3076	15	US-10-388-263-157	Sequence 157, App
19	78.6	39.7	3164	14	US-10-141-618-5	Sequence 5, Appli
20	78.6	39.7	3165	14	US-10-269-909-5	Sequence 5, Appli
21	78.6	39.7	3734	14	US-10-353-461-7	Sequence 7, Appli
22	78.6	39.7	5844	10	US-09-971-392-253	Sequence 253, App
23	78.6	39.7	5857	14	US-10-247-671-18	Sequence 18, Appli
24	78.6	39.7	6669	9	US-09-974-592-5	Sequence 5, Appli
25	74.4	37.6	1435	8	US-08-464-588-1	Sequence 1, Appli
26	74.4	37.6	1435	14	US-10-323-643-1	Sequence 199, App
27	74.4	37.6	2531	14	US-10-207-655-199	Sequence 7, Appli
28	74.4	37.6	2580	9	US-09-201-936-7	Sequence 1, Appli
29	74.4	37.6	2589	14	US-10-232-286-1	Sequence 337, App
30	74.4	37.6	3496	14	US-10-153-668-337	Sequence 3354, Ap
31	74.4	37.6	3532	9	US-09-880-107-3354	Sequence 1, Appli
32	74.4	37.6	3532	15	US-10-464-158-1	Sequence 7, Appli
33	74.4	37.6	3732	9	US-09-974-592-7	Sequence 19934, A
34	74.4	37.6	4614	10	US-09-814-353-19934	Sequence 13, Appl
35	71.2	36.0	2862	14	US-10-232-286-13	Sequence 13, Appl
36	71.2	36.0	3151	9	US-09-974-592-13	Sequence 131, App
37	71.2	35.9	7990	14	US-10-311-455-131	Sequence 7, Appli
38	71	35.9	7990	14	US-10-240-452-7	Sequence 11, Appl
39	70.6	35.7	2676	9	US-09-974-592-11	Sequence 41, Appl
40	69.6	35.2	2416	9	US-09-201-936-41	Sequence 39, Appl
41	69	34.8	2450	9	US-09-201-936-39	Sequence 1, Appli
42	59	29.8	3773	14	US-10-041-859-1	Sequence 132, App
C 43	56.6	28.6	7990	14	US-10-311-455-132	Sequence 8, Appli
C 44	56.6	28.6	7990	14	US-10-240-452-8	Sequence 1, Appli
45	54.6	27.6	5504	8	US-08-913-322-1	

ALIGNMENTS

RESULT 1

US-10-305-720-1053
; Sequence 1053, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1053
; LENGTH: 1659
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 GI016687
US-10-305-720-1053

Query Match	100.0%;	Score 198;	DB 15;	Length 1659;
Best Local Similarity	100.0%;	Pred. No. 5.9e-55;		
Matches 198;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	TATGAACAGCGATCTTTACTTTTGGGACATGATATCTCAGTTAACAGGAGCAGCTT	60	
Db	874	TATGAACAGCGATCTTTACTTTTGGGACATGATATCTCAGTTAACAGGAGCAGCTT	933	
QY	61	GCAAGAGCTGGATTTTATGCTTTAGGTGAGGTGATAAAGTAAAGTCTTCTCTGGA	120	
Db	934	GCAAGAGCTGGATTTTATGCTTTAGGTGAGGTGATAAAGTAAAGTCTTCTCTGGA	993	
QY	121	GGAGGCTTAAGTATGGAAGCCAGTGAAGACCTTGGGAAACAATGCTTAATGAT	180	
Db	994	GGAGGCTTAAGTATGGAAGCCAGTGAAGACCTTGGGAAACAATGCTTAATGAT	1053	

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QY 181 CCAGGTCGCAAAATATCTG 198
DB 1054 CCAGGTCGCAAAATATCTG 1071

RESULT 2
US-09-964-899-38
; Sequence 38, Application US/09964899
; Patent No. US2002017446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; CURRENT FILING DATE: 2001-09-27
; PRIOR FILING DATE: 2001-09-29
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-964-899-38

Query Match 100.0%; Score 198; DB 9; Length 2404;
Best Local Similarity 100.0%; Pred. No. 7e-55;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCATCTTTACTTTTGGGACATGGATATCTCAGTTAACAGGAGCAGCTT 60
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QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGAATAGTAAAGTCTTCACTGTGGA 120
DB 887 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGAATAGTAAAGTCTTCACTGTGGA 946

QY 121 GGAGGCTAACTGATTTGAAGCCCACTGAAGACCCCTTGGGACCAACATGCTAAATGGTAT 180
DB 947 GGAGGCTAACTGATTTGAAGCCCACTGAAGACCCCTTGGGACCAACATGCTAAATGGTAT 1006

QY 181 CCAGGTCGCAAAATATCTG 198
DB 1007 CCAGGTCGCAAAATATCTG 1024

RESULT 3
US-09-201-936-3
; Sequence 3, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)...(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-3

Query Match 100.0%; Score 198; DB 9; Length 2540;
Best Local Similarity 100.0%; Pred. No. 7.2e-55;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCATCTTTACTTTTGGGACATGGATATCTCAGTTAACAGGAGCAGCTT 60
DB 826 TATGAAGCAGCATCTTTACTTTTGGGACATGGATATCTCAGTTAACAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGAATAGTAAAGTCTTCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGAATAGTAAAGTCTTCACTGTGGA 945

QY 121 GGAGGCTAACTGATTTGAAGCCCACTGAAGACCCCTTGGGACCAACATGCTAAATGGTAT 180
DB 946 GGAGGCTAACTGATTTGAAGCCCACTGAAGACCCCTTGGGACCAACATGCTAAATGGTAT 1005

QY 181 CCAGGTCGCAAAATATCTG 198
DB 1006 CCAGGTCGCAAAATATCTG 1023

RESULT 4
US-10-007-926A-274
; Sequence 274, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOULGATTE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 274
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: baculoviral iap repeat-containing 4 (BIRC4)
; OTHER INFORMATION: Gene.
US-10-007-926A-274

Query Match 100.0%; Score 198; DB 14; Length 2540;
Best Local Similarity 100.0%; Pred. No. 7.2e-55;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCATCTTTACTTTTGGGACATGGATATCTCAGTTAACAGGAGCAGCTT 60
DB 826 TATGAAGCAGCATCTTTACTTTTGGGACATGGATATCTCAGTTAACAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGAATAGTAAAGTCTTCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGAATAGTAAAGTCTTCACTGTGGA 945
```

QY 121 GGAGGCTAACTGATTGGAGCCCACTGAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
DB 946 GGAGGCTAACTGATTGGAGCCCACTGAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
QY 181 CCAGGCTCAATATCTG 198
DB 1006 CCAGGCTCAATATCTG 1023

RESULT 5

US-09-974-592-3
; Sequence 3, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: 4623
; OTHER INFORMATION: n can be any nucleotide
; NAME/KEY: variation
; LOCATION: 4622
; OTHER INFORMATION: n can be any nucleotide
US-09-974-592-3

Query Match 100.0%; Score 198; DB 9; Length 5232;
Best Local Similarity 100.0%; Pred. No. 1e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAGCAGCATCTTTACTTTTGGGACATGGATATCTCAGTTAACAGGAGCAGCTT 60
DB 826 TATGAGCAGCATCTTTACTTTTGGGACATGGATATCTCAGTTAACAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGAATGAAGTAAAGTCTTCTCTGGA 120
DB 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGAATGAAGTAAAGTCTTCTCTGGA 945
QY 121 GAGGCTAACTGATTGAGCCCACTGAGACCCCTTGGGACCAACATGCTAAATGGTAT 180
DB 946 GGAGGCTAACTGATTGAGCCCACTGAGACCCCTTGGGACCAACATGCTAAATGGTAT 1005
QY 181 CCAGGCTCAATATCTG 198
DB 1006 CCAGGCTCAATATCTG 1023

RESULT 6

US-09-201-936-9
; Sequence 9, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E

; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-9

Query Match 87.4%; Score 173; DB 9; Length 2100;
Best Local Similarity 92.4%; Pred. No. 1.2e-46;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAGCAGCATCTTTACTTTTGGGACATGGATATCTCAGTTAACAGGAGCAGCTT 60
DB 916 TATGAGCAGCATCTTTACTTTTGGGACATGGATATCTCAGTTAACAGGAGCAGCTT 975
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGAATGAAGTAAAGTCTTCTCTGGA 120
DB 976 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGAATGAAGTAAAGTCTTCTCTGGA 1035
QY 121 GGAGGCTAACTGATTGAGCCCACTGAGACCCCTTGGGACCAACATGCTAAATGGTAT 180
DB 1036 GGAGGCTCAAGATTGAGACCCCTTGGGACCAACATGCTAAATGGTAT 1095
QY 181 CCAGGCTCAATATCT 197
DB 1096 CCAGGCTCAATATCT 1112

RESULT 7

US-09-974-592-9
; Sequence 9, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-974-592-9

Query Match 85.8%; Score 169.8; DB 9; Length 2691;
Best Local Similarity 91.4%; Pred. No. 1.6e-45;
Matches 180; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTACTTTTGGACATGATATCTCACTTAAACAAGGAGCAGCTT 60
DB 1461 TATGAAGCAGGATCGTGTACTTTTGGACATGATATCTCACTTAAACAAGGAGCAGCTT 1520

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
DB 1521 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 1580

QY 121 GGAGGCTAACTGATTCGAGCCAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 180
DB 1581 GGAGGCTCAAGGATTCGAGCCAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 1640

QY 181 CCAGGGTCAAAATATCT 197
DB 1641 CCAGGGTCAAAATACCT 1657

RESULT 8
US-10-095-407-16/c
; Sequence 16, Application US/10095407
; Publication No. US20020164330A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/10/095,407
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/091,650
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/054,646
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 152331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
US-10-095-407-16

Query Match 79.7%; Score 157.8; DB 13; Length 152331;
Best Local Similarity 90.4%; Pred. No. 9.2e-41;
Matches 179; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 1 TATGAAGCAGGATCTTACTTTTGGACATGATATCTCACTTAAACAAGGAGCAGCTT 60
DB 3298 TATGAAGCAGGATCATTTACTTTTGGATGTGGATATATTCAGTTAAACAAGGAGCAGCTT 3239

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
DB 3238 TCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 3179

QY 121 GGAGGCTAACTGATTCGAGCCAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 180
DB 3178 GGAGGCTAACTGATTCGAGCCAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 3120

QY 181 CCAGGGTCAAAATATCTG 198
DB 3119 CCAGGGTCAAAATATCTG 3102

RESULT 9
US-10-095-407-17
; Sequence 17, Application US/10095407
; Publication No. US20020164330A1

GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/10/095,407
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/091,650
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/054,646
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
US-10-095-407-17

Query Match 66.4%; Score 131.4; DB 13; Length 176373;
Best Local Similarity 95.7%; Pred. No. 5.3e-32;
Matches 135; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 58 CTTCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGT 117
DB 12549 CTTTCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGT 12608

QY 118 GGAGGAGGCTAACTGATTCGAGCCAGTGAAGCCCTTGGGAACAACATGCTAAATGG 177
DB 12609 GGAGGAGGCTAACTGATTCGAGCCAGTGAAGCCCTTGGGAACAACATGCTAAATGG 12668

QY 178 TATCCAGGCTGCAAAATATCTG 198
DB 12669 CATCCAGGCTGCAAAATATCTG 12689

RESULT 10
US-10-102-524-906/c
; Sequence 906, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Gaiger, Alexander
; APPLICANT: Gordon, Brian
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER
; FILE REFERENCE: 210121.572
; CURRENT APPLICATION NUMBER: US/10/102,524
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 1863
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 906
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-102-524-906

Query Match 39.7%; Score 78.6; DB 14; Length 255;
Best Local Similarity 68.8%; Pred. No. 8.2e-16;
Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 42 AGTTAAACAAGGAGCAGCTTGAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGT 101
DB 223 AGTTAACTCTGAGCAGCTTGAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGT 164

QY 102 AAAGTCTTCACTGTGAGGAGGCTTAAGTGAAGCCCAAGTGAAGACCCCTTGGGA 161

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Db 163 CAATGCTTTTGTGTGATGGTGAAGTCAAGTCTGGATCTGGAGATGATCCATGGGT 104
QY 162 ACAACATGCTAAATGGTATCAGGGTCAAAATATCTG 198
Db 103 TCAACATGCCAAGTGGTTTCCAGGTGTGAGTACTTG 67

RESULT 11
US-10-305-720-1076
; Sequence 1076, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1076
; LENGTH: 2563
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g1160974
US-10-305-720-1076

Query Match 39.7%; Score 78.6; DB 15; Length 2563;
Best Local Similarity 68.8%; Pred. No. 2.3e-15;
Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 42 AGTTAAACAGGACAGCTTGCAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGT 101
Db 932 AGTTAATCCTGAGCAGCTTGCAGTGCAGGTTTATATGTTGGTTAACAGTATGATCT 991
QY 102 AAAGTCTTTCACCTGTGAGAGGGCTAACTGATGGAAGCCAGTGAAGACCCCTTGGGA 161
Db 992 CAAATGCTTTTGTGTGATGGTGAAGTCTCAGGTGTTGGGAATCTGGAGATGATCCATGGT 1051
QY 162 ACAACATGCTAAATGGTATCAGGGTGCAAATATCTG 198
Db 1052 TCAACATGCCAAGTGGTTTCCAGGTGTGAGTACTTG 1088

RESULT 12
US-10-232-286-3
; Sequence 3, Application US/10232286
; Publication No. US20030143579A1
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/232,286
; FILING DATE: 30-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US/08/569,749
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-232-286-3

Query Match 39.7%; Score 78.6; DB 14; Length 2601;
Best Local Similarity 68.8%; Pred. No. 2.4e-15;
Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 42 AGTTAAACAGGACAGCTTGCAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGT 101
Db 932 AGTTAATCCTGAGCAGCTTGCAGTGCAGGTTTATATGTTGGTTAACAGTATGATCT 991
QY 102 AAAGTCTTTCACCTGTGAGAGGGCTAACTGATGGAAGCCAGTGAAGACCCCTTGGGA 161
Db 992 CAAATGCTTTTGTGTGATGGTGAAGTCTCAGGTGTTGGGAATCTGGAGATGATCCATGGT 1051
QY 162 ACAACATGCTAAATGGTATCAGGGTGCAAATATCTG 198
Db 1052 TCAACATGCCAAGTGGTTTCCAGGTGTGAGTACTTG 1088

RESULT 13
US-09-201-936-5
; Sequence 5, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2676
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2470)...(2470)
; OTHER INFORMATION: N may be any nucleotide
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2476)...(2476)
; OTHER INFORMATION: N may be any nucleotide
; FEATURE:
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NAME/KEY: variation
LOCATION: (2483)...(2483)
OTHER INFORMATION: N may be any nucleotide
FEATURE:
NAME/KEY: variation
LOCATION: (2602)...(2602)
OTHER INFORMATION: N may be any nucleotide
US-09-201-936-5

Query Match 39.7%; Score 78.6; DB 9; Length 2676;
Best Local Similarity 68.8%; Pred. No. 2.4e-15;
Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 42 AGTTAAACAGGACGCTTGAAGAGCTGGATTTTATGCTTTAGCTGAAGGTGATAAGT 101
DB 998 AGTTAACTCTGAGCAGCTTGAAGTGGGGTTTTTATGCTGGTGAACAGTATGATGT 1057
QY 102 AAAGTGCCTTCACTGTGAGGAGGCTTAACCTGATTGGAAGCCAGTGAAGACCCCTTGGGA 161
DB 1058 CAAATGCTTTTCTGTGTGATGTGGACTCAGGTGTGGGAATCTGGAGATGATCCATGGGT 1117
QY 162 ACAACATGCTAAATGGTATCCAGGTGCAATATCTG 198
DB 1118 TCAACATGCCAAGTGGTTTCCAAGGTGTGAGTACTTG 1154

RESULT 14

US-10-240-425-1436
Sequence 1436, Application US/10240425
Publication No. US20040033502A1

GENERAL INFORMATION:

APPLICANT: Williams, Amanda
APPLICANT: Bolland, Joseph F.
APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
APPLICANT: Wetzel, Jon C.
APPLICANT: Scherif, Uwe
APPLICANT: Vockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
FILE REFERENCE: 44921-5026
CURRENT APPLICATION NUMBER: US/10/240,425
PCT/US01/09847

PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 1436
LENGTH: 2916
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: Genbank Accession No. US20040033502A1 U45878
FEATURE:
NAME/KEY: unsure

LOCATION: (1) (2907)

OTHER INFORMATION: n = a or c or g or t

US-10-240-425-1436

Query Match 39.7%; Score 78.6; DB 12; Length 2916;
Best Local Similarity 68.8%; Pred. No. 2.5e-15;
Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 42 AGTTAAACAGGACGCTTGAAGAGCTGGATTTTATGCTTTAGCTGAAGGTGATAAGT 101
DB 1258 AGTTAACTCTGAGCAGCTTGAAGTGGGGTTTTTATGCTGGTGAACAGTATGATGT 1317
QY 102 AAAGTGCCTTCACTGTGAGGAGGCTTAACCTGATTGGAAGCCAGTGAAGACCCCTTGGGA 161
DB 1318 CAAATGCTTTTCTGTGTGATGTGGACTCAGGTGTGGGAATCTGGAGATGATCCATGGGT 1377
QY 162 ACAACATGCTAAATGGTATCCAGGTGCAATATCTG 198

DB 1378 TCAACATGCCAAGTGGTTTCCAAGGTGTGAGTACTTG 1414

RESULT 15

US-09-954-456-1635
Sequence 1635, Application US/09954456
Patent No. US20020115057A1

GENERAL INFORMATION:

APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR FILING DATE: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: Patent in version 3.0
SEQ ID NO 1635
LENGTH: 3076
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-1635

Query Match 39.7%; Score 78.6; DB 9; Length 3076;

Best Local Similarity 68.8%; Pred. No. 2.5e-15;
Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 42 AGTTAAACAGGACGCTTGAAGAGCTGGATTTTATGCTTTAGCTGAAGGTGATAAGT 101
DB 1534 AGTTAACTCTGAGCAGCTTGAAGTGGGGTTTTTATGCTGGTGAACAGTATGATGT 1593
QY 102 AAAGTGCCTTCACTGTGAGGAGGCTTAACCTGATTGGAAGCCAGTGAAGACCCCTTGGGA 161
DB 1594 CAAATGCTTTTCTGTGTGATGTGGACTCAGGTGTGGATCTGGAGATGATCCATGGGT 1653
QY 162 ACAACATGCTAAATGGTATCCAGGTGCAATATCTG 198
DB 1654 TCAACATGCCAAGTGGTTTCCAAGGTGTGAGTACTTG 1690

Search completed: March 13, 2004, 06:34:00
Job time : 210 secs

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OM nucleic - nucleic search, using sw model

Run on: March 13, 2004, 04:02:03 ; Search time 2177.5 Seconds

(without alignments)
2715.367 Million cell updates/sec

Title: US-09-654-743-47

Perfect score: 198

Sequence: 1 taagaacacggatctttac.....atccagggtgcaaatatctg 198

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em_estba:.*
2: em_esthum:.*
3: em_estin:.*
4: em_estmu:.*
5: em_estov:.*
6: em_estpl:.*
7: em_estro:.*
8: em_hcc:.*
9: gb_est1:.*
10: gb_est2:.*
11: gb_hcc:.*
12: gb_est3:.*
13: gb_est4:.*
14: gb_est5:.*
15: em_estfun:.*
16: em_estom:.*
17: em_gss_hum:.*
18: em_gss_inv:.*
19: em_gss_pln:.*
20: em_gss_vrt:.*
21: em_gss_fun:.*
22: em_gss_mam:.*
23: em_gss_mus:.*
24: em_gss_pro:.*
25: em_gss_rod:.*
26: em_gss_phg:.*
27: em_gss_vrl:.*
28: gb_gss1:.*
29: gb_gss2:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	166	83.8	1805	11	BC039318 Homo sapi
2	166	83.8	1851	11	BC056914 Homo sapi
3	164.6	83.1	773	14	CD350778 UI-M-G10-
4	164.4	83.0	1789	11	BC046168 Homo sapi

C	5	157.4	79.5	628	9	AI573382
	6	114	57.6	1177	12	BM805359
	7	112	56.6	536	9	AUI23207
	8	104.4	52.7	716	9	AV706807
C	9	100.2	50.6	318	10	BF659610
	10	99	50.0	617	10	BF663325
C	11	96.4	48.7	721	29	CE100865
	12	94.4	47.7	504	10	BB650856
C	13	91.6	46.3	334	12	BM220130
C	14	91.6	46.3	584	13	BQ552032
	15	90.8	45.9	791	14	CF222542
C	16	87	43.9	420	28	AQ011995
	17	85	42.9	1494	29	AY398943
	18	84	42.4	849	28	BZ242580
	19	80.6	40.7	373	13	BU662508
	20	79.4	40.1	663	13	BU658508
	21	78.6	39.7	341	10	AK375598
	22	78.6	39.7	354	10	AK375594
	23	78.6	39.7	402	10	AK846507
	24	78.6	39.7	531	10	AK375599
	25	78.6	39.7	532	10	AK846425
	26	78.6	39.7	546	10	AK846421
	27	78.6	39.7	571	10	AK375649
C	28	78.6	39.7	582	10	AK846337
	29	78.6	39.7	590	10	BZ268377
	30	78.6	39.7	621	10	AK375648
	31	78.6	39.7	680	10	AK375625
	32	78.6	39.7	886	13	BQ652590
	33	78.6	39.7	1472	29	AY398945
	34	78.6	39.7	1799	29	AV420753
	35	78.4	39.6	269	10	BZ506790
	36	74.4	37.6	441	12	BM312708
C	37	74.4	37.6	563	9	AA702174
	38	74.4	37.6	652	9	AV704923
	39	74.4	37.6	831	13	BU935186
	40	74.4	37.6	851	12	B1253303
	41	74.4	37.6	896	13	BQ439248
	42	74.4	37.6	917	13	BU928804
	43	74.4	37.6	1084	13	BU902159
	44	74.2	37.5	690	29	CB697566
	45	74	37.4	354	9	AA354707

ALIGNMENTS

RESULT 1
BC039318
LOCUS
DEFINITION Homo sapiens, Similar to baculoviral IAP repeat-containing 8, clone
INAGR:5369405, mRNA.
ACCESSION BC039318
VERSION BC039318.1 GI:25058167
KEYWORDS HTc.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Strausberg R.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: gcgaps-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome

BC039318 Homo sapiens, Similar to baculoviral IAP repeat-containing 8, clone
INAGR:5369405, mRNA.
ACCESSION BC039318
VERSION BC039318.1 GI:25058167
KEYWORDS HTc.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Strausberg R.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: gcgaps-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-sgsc.stanford.edu>
 Contact: (Dickson, Mark) mcdpaxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 74 Row: h Column: 10
 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein
 This clone has the following problem: frame shifted.

FEATURES

source

1. 1805
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5269405"
 /tissue_type="Testis"
 /clone_lib="NIH MGC_97"
 /lab_host="DH10B"
 /note="Vector: pBluescript"

ORIGIN

Query Match 83.8%; Score 166; DB 11; Length 1805;
 Best Local Similarity 89.9%; Pred. No. 3e-40;
 Matches 178; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGATCTTTACTTTTGGACATGGATATCTCAGTTTAAAGGAGCAGCTT 60
 Db 1028 TATGAGCCCGGCTCACTTCTTTGGACATGGATATCTCAGTTTAAAGGAGCAGCTT 1087

QY 61 GCAAGAGCTGGATTTATCTTTAGCTGAAGGTGATAAGTAAAGTCTTCTACTGTGGA 120
 Db 1088 GCAAGAGCTGGATTTATCTTTAGCTGAAGGTGATAAGTAAAGTCTTCTACTGTGGA 1147

QY 121 GGAGGCTTAACGATCTGGAGCCAGTGAAGACCTTGGGACACACATGTAATGTAT 180
 Db 1148 GGAGGCTTAGCCAACTGGAGCCCAAGGAAGATCTTTGGGACACACATGTAATGTAT 1207

QY 181 CCAGGCTGCAATATCTG 198
 Db 1208 CCAGGCTGCAATATCTG 1225

RESULT 2

BC056914

LOCUS

DEFINITION Homo sapiens baculoviral IAP repeat-containing 8, mRNA HTC 16-SEP-2003
 IMAGE:5742924.

ACCESSION

BC056914.1 GI:34784469

VERSION

HTC.

KEYWORDS

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1851)

Strausberg,R.L., Peingold,E.A., Grouse,L.H., Derge,J.G.,

Klausner,R.D., Collins,F.S., Wagner,L., Sherman,C.M., Schuler,G.D.,

Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Shat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heien,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,

Carninci,P., Frange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Villalon,D.K., Muzny,D.M., Sodergren,S.J., Lu,X., Gibbs,R.A.,

Fahey,J., Helton,E., Kettman,M., Madan,A., Young,A.C., Shevchenko,Y.,

Buffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
 Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E.,
 Butterch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,

Suanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,

Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo

Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven

Ness, Pawan Pandoh, Anna-Liisa Prabhhu, Parvaneh Saedi, Jacqueline

Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stott,

Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,

George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 119 Row: h Column: 2

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 16974127

This clone has the following problem: retained intron.

FEATURES

source

1. 1851
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5742924"
 /tissue_type="Brain, adult medulla"
 /clone_lib="NIH MGC_119"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 83.8%; Score 166; DB 11; Length 1851;
 Best Local Similarity 89.9%; Pred. No. 3e-40;
 Matches 178; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGATCTTTACTTTTGGACATGGATATCTCAGTTTAAAGGAGCAGCTT 60
 Db 1062 TATGAGCCCGGCTCACTTCTTTGGACATGGATATCTCAGTTTAAAGGAGCAGCTT 1121

QY 61 GCAAGAGCTGGATTTATCTTTAGCTGAAGGTGATAAGTAAAGTCTTCTACTGTGGA 120
 Db 1122 GCAAGAGCTGGATTTATCTTTAGCTGAAGGTGATAAGTAAAGTCTTCTACTGTGGA 1181

QY 121 GGAGGCTTAACGATCTGGAGCCAGTGAAGACCTTGGGACACACATGTAATGTAT 180
 Db 1182 GGAGGCTTAGCCAACTGGAGCCCAAGGAAGATCTTTGGGACACACATGTAATGTAT 1241

QY 181 CCAGGCTGCAATATCTG 198
 Db 1242 CCAGGCTGCAATATCTG 1259

```

RESULT 3
CD350778      773 bp      mRNA      linear      EST 09-JUL-2003
LOCUS          UI-M-GIO-cgh-g-23-0-UI.r1 NIH_BMAP_GIO Mus musculus cDNA clone
DEFINITION     IMAGE:6853392.5', mRNA sequence.
ACCESSION      CD350778
VERSION        CD350778.1 GI:31142365
KEYWORDS       EST.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 773)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
Location/Qualifiers
1. 773
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6853392"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_GIO"
/notes="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP). Gene Discovery in the
Developing Mouse Nervous System, supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN
Query Match      83.1%; Score 164.6; DB 14; Length 773;
Best Local Similarity 92.5%; Pred. No. 5.7e-40;
Matches 173; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 11 GGATCTTTACTTTGGGACATGGATATACTACTGATTAAACAGAGAGAGCTTGCAGAGCTG 70
|||||
Db 1 GGATCGTTACTTTTGGACATGGACATCCTCAGTTAAACAGAGAGAGCTTGCAGAGCTG 60

QY 71 GATTTTATGCTTTAGTGAAGGTGATTAAGTAAAGTCTTTCACTGTGGAGGAGGCTAA 130
|||||
Db 61 GATTTTATGCTTTAGTGAAGGTGATTAAGTGAAGTCTTTCACTGTGGAGGAGGCTCA 120

QY 131 CTGATTGGAAGCCCAAGTGAAGACCCCTTGGGAACAACTGCTAAATGCTATCCAGGGTGCA 190
|||||
Db 121 CGGATTGGAAGCCCAAGTGAAGACCCCTTGGGAACAACTGCTAAATGCTATCCAGGGTGCA 180

QY 191 AATATCT 197
|||||

```

```

Db 181 AATACT 187

RESULT 4
BC046168      1789 bp      mRNA      linear      HTC 13-FEB-2003
LOCUS          BC046168
DEFINITION     Homo sapiens, similar to baculoviral IAP repeat-containing 8, clone
ACCESSION      BC046168
VERSION        BC046168.1 GI:28374455
KEYWORDS       HTC.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1789)
Strausberg,R.
Direct Submission
Submitted (31-JAN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAX Plate: 107 Row: i Column: 1
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein
This clone has the following problem: frame shifted.

FEATURES
Location/Qualifiers
1. 1789
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5742590"
/tissue_type="Brain, adult medulla"
/clone_lib="NIH_MGC_119"
/lab_host="DH10E"
/notes="Vector: pCMV-SPORT6"

ORIGIN
Query Match      83.0%; Score 164.4; DB 11; Length 1789;
Best Local Similarity 89.4%; Pred. No. 9.4e-40;
Matches 177; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 TATGAACACGGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAGAGAGCTT 60
|||||
Db 1002 TATGAACCCGGCTCATTTACTTTTGGGACATGGATATCTCCTGTCACAGAGAGCTT 1061

QY 61 GCAAGAGCTGGATTTTATGCTTTTAGTGAAGGTGATAAAGTAAAGTCTTCACTGTGA 120
|||||
Db 1062 GCAAGAGCTGGATTTTATGCTTTTAGTGAAGGTGATAAAGTAAAGTCTTCACTGTGA 1121

QY 121 GGAGGGTAACTGATTTGGAGCCCGAGTGAAGACCCCTTGGGAACAACTGCTAAATGCTAT 180
|||||
Db 1122 GGAGGGTAACTGATTTGGAGCCCGAGTGAAGACCCCTTGGGAACAACTGCTAAATGCTAT 1181

QY 181 CCAGGGTGCAAAATATCTG 198
|||||
Db 1182 CCAGGGTGCAAAATATCTG 1199

```


JOURNAL
COMMENT

Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5', & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES

source

1..536
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RM1000921"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_lib="NT2RM1"
/note="Vector: pUC19FL3; mRNA from uninduced NT2 neuronal
precursor cells"

ORIGIN

Query Match 56.6%; Score 112; DB 9; Length 536;
Best Local Similarity 98.2%; Pred. No. 9.4e-24;
Matches 112; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 85 GGTGAAGTGATAAGTAAAGTCTTTCACCTGGAGGAGGCTAACTGATTGGAGCCCC 144
DB 99 GGTGAAGTGATAAGTAAAGTCTTTCACCTGGAGGAGGCTAACTGATTGGAGCCCC 158
QY 145 AGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAAATATCTG 198
DB 159 AGTGAANACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAAATATCTG 212

RESULT 8

AV706807

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AV706807 ADB Homo sapiens cDNA clone ADBCOF01 5', mRNA sequence.
AV706807
AV706807.1 GI:10724085

EST.
Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 716)

Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G.,

Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z.,

Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S.,

Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z. and Han, Z.

Homo sapiens cDNA ADB clones

Unpublished (2000)

Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801919 (ex. 45)

Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

Location/Qualifiers

1..716

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="ADBCOF01"

/tissue_type="Adrenal gland"

/dev_stage="Adult"

/lab_host="SOLR"

ORIGIN

Query Match 52.7%; Score 104.4; DB 9; Length 716;
Best Local Similarity 94.7%; Pred. No. 2.4e-21;
Matches 108; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 85 GGTGAAGTGATAAGTAAAGTCTTTCACCTGGAGGAGGCTAACTGATTGGAGCCCC 144
DB 156 GGTGAAGTGATAAGTAAAGTCTTTCACCTGGAGGAGGCTAACTGATTGGAGCCCC 215
QY 145 AGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAAATATCTG 198
DB 216 AGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAAATATCTG 269

RESULT 9

BF659610/c

LOCUS

DEFINITION

BF659610.1 GI:11924744

EST.

Mus musculus

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 318)

NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbe@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CCGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

image.llnl.gov/image/html/iresources.shtml

MGI:1436942

Possible reversed clone: polyT not found

Seq primer: -40UP from Gibco

High quality sequence stop: 226.

Location/Qualifiers

1..318

/organism="Mus musculus"

/mol_type="mRNA"

/strain="Czech 11"

/db_xref="taxon:10090"

/clone="IMAGE:3676174"

/tissue_type="spontaneous tumor, metastatic to mammary.

Stem cell origin."

/lab_host="DH10B"

/clone_lib="NCI-CCGAP Lu29"

/note="Organ: lung; Vector: pCMV-Sport6; Site 1: Salt;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigator

providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 50.6%; Score 100.2; DB 10; Length 318;
Best Local Similarity 92.9%; Pred. No. 3.4e-20;
Matches 105; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 53 AGCAGCTTGCAGAGCTGGATTCTTTATCTTAGTGTAAGGTATAAGTAAGTGTCTTC 112

```

Db 317 AGCAGCTTGAAGAGTTGGATTTTAAGCTTTAGTGTGAAGCGGATAAAGTCAAGTCTTTC 258
113 ACTGTGGAGGAGGCTAATCTGATTTGGAGCCCAAGTGAAGCCCTTGGACAA 165
Db 257 ACTGTGGAGGAGGCTCTCGGATTTGGAGCCCAAGTGAAGCCCTTGGACAA 205

RESULT 10
LOCUS BB663325 617 bp mRNA linear EST 26-OCT-2001
DEFINITION BB663325 RIKEN full-length enriched, 15 days embryo head Mus
ACCESSION BB663325
VERSION BB663325
KEYWORDS BB663325.1 GI:16497079
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 617)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
FEATURES
Location/Qualifiers
1..617
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/mol_type="mRNA"
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genomic Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGGATCCCAAGAGCTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5',
GAGAGAGAGATCTCGATTAAATTAATTAATCCCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I"
ORIGIN
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Best Local Similarity 87.8%; Pred.No. 1e-19;
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Db 108 TGCACCTAAGTGTGAAGCGGATTAAGTGAAGTCTTCACTGTGGAGGAGGGCTCACGGA 167
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QY 195 TCT 197
Db 228 CCT 230

RESULT 11
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DEFINITION tigr-gss-dog-17000371110448 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE100865
VERSION CE100865.1 GI:35167750
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 721)
Kirkness,E.F., Hafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
22875432
14512627
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
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[illegible]

ACCESSION BB650856.1
VERSION BB650856.1 GI:16485110

EST.
Mus musculus (house mouse)

SOURCE	ORGANISM	Mus musculus	Mus musculus (house mouse)	Mus musculus (mouse)
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			

REFERENCE
1 (bases 1 to 504)
Arakawa, T., Carrincci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
AUTHORS

HARA, A., HIRANO, K., HORI, F., ISHII, Y., ITO, M., KAWAI, J., KANO, H., KODA, M., KOYE, S., MATSUYAMA, T., MIYAZAKI, A., NOMURA, K., OHNO, M., OKAZAKI, Y., OKIDO, T., SAITO, R., SAKAI, C., SAKAI, K., SANO, H., SASAKI, D., SHIBATA, K., SHINAGAWA, A., SHIRAKI, T., SUGABE, Y., SUZUKI, H., TAGAMI, M., TAGAWA, A., TAKAHASHI, F., TAKEDA, Y., TANAKA, T., TOYA, T., MURAMATSU, M. and HAYASHIZAKI, Y. RIKEN Mouse ESs (Arakawa, T., et al. 2001)

JOURNAL
 COMMENT
 Dispublished (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216

E-mail: genome-res@esc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. *Genome Res.* 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Watanahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K.,
 Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
 and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11): 1757-1771 (2000)

Komno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001).
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. *Mamm. Genome* 12, 673-677 (2001).
Please visit our web site (<http://genome.gen.riken.go.jp>) for
further details.
e mouse tissues.

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DEFINITION	C0935E08-3 NIA Mouse 12.5-dpc Male Genital Ridge/Mesonephros cDNA Library (long) Mus musculus cDNA clone NIA:C0935E08 IMAGE:30037975 3' mRNA sequence.				

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VERSION	BM220130.2	GI:31478783	
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ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 334)		

AUTHORS	Piao, Y., KO, N. T., Lim, M. K. and KO, M. S. H.
TITLE	Construction of long-transcript enriched cDNA libraries from subprogram amounts of total RNAs by a universal PCR amplification method
JOURNAL	Genome Res. 11 (9), 1553-1558 (2001)

21429068
 MEDLINE
 PUBLISHED
 COMMENT
 On Dec 14, 2001 this sequence version replaced gi:17780130.
 Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6620, USA
 Email: cdna@igsun.grc.nia.nih.gov
 Plate: C0935 row: E column: 08
 Seq primer: -21M13 Forward
 High quality sequence stop: 334

POLYA=Yes
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 5'-TGACTAGTCTAGATCGGAGCGCCGCTTTT-3' from 1.8 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L1-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.4 kb. The library was constructed by Yulan Piao (NIA)."
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 Mus musculus
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 1 (bases 1 to 584)
 VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G., Martin, P.R., Stagg, C.A., Bassey, U., Aiba, K., Hamatani, T., Kargul, G.J., Luo, A.G., Kelso, J., Hide, W. and Ko, M.S.H.
 Assembly, verification, and initial annotation of NIA 7.4K mouse cDNA clone set
 Genome Res. 12 (12), 1999-2003 (2002)
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 12466305
 BQ552032
 H4013A06-3 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
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 BQ552032
 EST.
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 Assembly, verification, and initial annotation of NIA 7.4K mouse cDNA clone set
 Genome Res. 12 (12), 1999-2003 (2002)
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 Silurana tropicalis (western clawed frog)
 Silurana tropicalis
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 1 (bases 1 to 791)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgsaps-remail.nih.gov
 Tissue Procurement: Robert M. Grainger
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L14W14642 row: f column: 21
 High quality sequence start: 3
 COMMENT
 Other ESTs: H4013A06-5
 Contact: Yong Qian
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
 Email: cdna@lgsun.grc.nia.nih.gov
 This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7.4k.html for details.
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 Query Match 46.3%; Score 91.6; DB 13; Length 584;
 Best Local Similarity 91.5%; Pred. No. 2e-17;
 Matches 97; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 82 TTAGTGAAGTGAATAAGTAAAGTCTTCACTGTGGAGGAGGCTAACTGATTGGAAG 141
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 QY 142 CCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGT 187
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 RESULT 15
 CF222542
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 DEFINITION
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 VERSION
 KEYWORDS
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 Silurana tropicalis (western clawed frog)
 Silurana tropicalis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Silurana.
 1 (bases 1 to 791)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgsaps-remail.nih.gov
 Tissue Procurement: Robert M. Grainger
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
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Xenopus Gene Collection (XGC) library."

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Query Match 45.9%; Score 90.8; DB 14; Length 791;
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Matches 131; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
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Qy 121 GGAGGCTTAAGTGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db 387 GGAGTGTAAATTTGTTGTCGGCAACAGATGATCCTTGGGAGAGCATGCCAAGGCATAT 446
Qy 181 CCAGGTCGAATATCTG 198
Db 447 CCTGATGCAAGTTCCTG 464

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Job time : 2184.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 13, 2004, 00:37:57 ; Search time 1045.5 Seconds
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Title: US-09-654-743-51

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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4	194.8	98.4	2691	6	AR106400	Sequence
5	194.8	98.4	2691	6	AR116702	Sequence
6	194.8	98.4	2691	6	AR370620	Sequence
7	194.8	98.4	2691	6	AX670906	Sequence
8	194.8	98.4	2691	6	BD190871	Detection
9	194.8	98.4	2691	10	MMUS8990	Mus musculus
10	186.8	94.3	1988	10	MMU36842	Mus musculus
11	185.2	93.5	205991	2	AC109227	Sequence
12	185.2	93.5	208236	2	AC137152	Sequence
13	182	91.9	1491	10	AF183429	Rattus no
14	182	91.9	2468	10	AB033366	Rattus no
15	182	91.9	3032	10	AF304334	Rattus no
16	180.4	91.1	2032	10	AF304333	Rattus no
17	173	87.4	1588	6	AR263641	Sequence
18	173	87.4	1659	6	E31042	Method for
19	173	87.4	1659	6	AR270490	Sequence
20	173	87.4	1659	9	HSU32974	Human IAP-1
21	173	87.4	2086	9	BC032729	Homo sapi
22	173	87.4	2404	6	AX429575	Sequence
23	173	87.4	2540	6	AR103281	Sequence
24	173	87.4	2540	6	AR302736	Sequence
25	173	87.4	2540	6	AR380355	Sequence
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27	173	87.4	2540	6	AX412118	Sequence
28	173	87.4	2540	6	AX587804	Sequence
29	173	87.4	2540	9	HSU45880	Human X-11n
30	173	87.4	3000	6	AX412131	Sequence
31	173	87.4	5232	6	AR106397	Sequence
32	173	87.4	5232	6	AR116699	Sequence
33	173	87.4	5232	6	AX670900	Sequence
34	173	87.4	5232	6	BD190868	Detection
35	173	79.3	1752	6	AX104956	Sequence
36	157	79.3	1752	6	AX164681	Homo sapi
37	157	79.3	1752	9	AC079753	Homo sapi
38	157	79.3	154214	9	AC079753	Homo sapi
39	149	75.3	1758	6	AX370787	Sequence
40	149	75.3	1758	6	AX370789	Sequence
41	149	75.3	4993	6	AX104968	Sequence
42	149	75.3	4993	9	AF164682	Homo sapi
43	149	75.3	144301	9	AC010467	Homo sapi
44	149	75.3	165662	9	AC092070	Homo sapi
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ALIGNMENTS

RESULT 1	AR302739	AR302739	2100 bp	DNA	linear	PAT 12-JUN-2003
LOCUS	Sequence 9 from patent US 6541457.					
DEFINITION	Sequence 9 from patent US 6541457.					
ACCESSION	AR302739					
VERSION	AR302739.1	GI:31691182				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 2100)					
AUTHORS	Korneluk,R.G., MacKenzie,A.E., Baird,S. and Liston,P.					
TITLE	Mammalian IAP gene family, primers, probes and detection methods					
JOURNAL	Patent: US 6541457-A 9 01-APR-2003;					
FEATURES	Location/Qualifiers					

QY 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGAGCCAGCATGCTAAGTGTCTAC 180
Db 1581 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGAGCCAGCATGCTAAGTGTCTAC 1640

QY 181 CCAGGGTGCAAAATACCTA 198
Db 1641 CCAGGGTGCAAAATACCTA 1658

RESULT 5
AR116702
LOCUS AR116702 2691 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 9 from patent US 6133437.
ACCESSION AR116702
VERSION AR116702.1 GI:14097024
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2691)
AUTHORS Korneluk,R.G., Mackenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and Pratt,C.
TITLE Modulation of IAPs for the treatment of proliferative diseases
JOURNAL Patent: US 6133437-A 9 17-OCT-2000;
FEATURES Location/Qualifiers
source 1. .2691
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 98.4%; Score 194.8; DB 6; Length 2691;
Best Local Similarity 99.0%; Pred. No. 1e-44;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAGGAGCAGCTT 60
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QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGA 120
Db 1521 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGA 1580

QY 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGAGCCAGCATGCTAAGTGTCTAC 180
Db 1581 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGAGCCAGCATGCTAAGTGTCTAC 1640

QY 181 CCAGGGTGCAAAATACCTA 198
Db 1641 CCAGGGTGCAAAATACCTA 1658

RESULT 6
AR370620
LOCUS AR370620 2691 bp DNA linear PAT 12-SBP-2003
DEFINITION Sequence 9 from patent US 6300492.
ACCESSION AR370620
VERSION AR370620.1 GI:34607376
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2691)
AUTHORS Korneluk,R.G., Mackenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and Pratt,C.
TITLE Modulation of IAPs for the diagnosis and antisense treatment of proliferative disease
JOURNAL Patent: US 6300492-A 9 09-OCT-2001;
FEATURES Location/Qualifiers
source 1. .2691
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 98.4%; Score 194.8; DB 6; Length 2691;
Best Local Similarity 99.0%; Pred. No. 1e-44;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAGGAGCAGCTT 60
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QY 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGAGCCAGCATGCTAAGTGTCTAC 180
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QY 181 CCAGGGTGCAAAATACCTA 198
Db 1641 CCAGGGTGCAAAATACCTA 1658

RESULT 7
AX670906 2691 bp DNA linear PAT 27-MAR-2003
LOCUS AX670906 Sequence 9 from Patent EP1277836.
DEFINITION AX670906
ACCESSION AX670906
VERSION AX670906.1 GI:29329409
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Korneluk,R., Mackenzie,A.E., Liston,P., Baird,S., Tsang,B. and Pratt,C.
TITLE Modulation of the iaps and naip for the treatment of proliferative diseases
JOURNAL Patent: EP 1277836-A 9 22-JAN-2003;
UNIVERSITY OF OTTAWA (CA)
LOCATION/Qualifiers
source 1. .2691
/organism="Mus musculus"
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ORIGIN
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Best Local Similarity 99.0%; Pred. No. 1e-44;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAGGAGCAGCTT 60
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Db 1521 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGA 1580

QY 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGAGCCAGCATGCTAAGTGTCTAC 180
Db 1581 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGAGCCAGCATGCTAAGTGTCTAC 1640

QY 181 CCAGGGTGCAAAATACCTA 198
Db 1641 CCAGGGTGCAAAATACCTA 1658

RESULT 8
BD190871 2691 bp DNA linear PAT 17-JUL-2003
LOCUS BD190871
DEFINITION Detection and modulation of the IAPs and NAIP for the diagnosis and treatment of proliferative disease.
FEATURES
source BD190871
ACCESSION BD190871

Query Match 98.4%; Score 194.8; DB 6; Length 2691;
Best Local Similarity 99.0%; Pred. No. 1e-44;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAGGAGCAGCTT 60
Db 1461 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAGGAGCAGCTT 1520

QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGA 120
Db 1521 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGA 1580

QY 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGAGCCAGCATGCTAAGTGTCTAC 180
Db 1581 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGAGCCAGCATGCTAAGTGTCTAC 1640

QY 181 CCAGGGTGCAAAATACCTA 198
Db 1641 CCAGGGTGCAAAATACCTA 1658

RESULT 7
AX670906 2691 bp DNA linear PAT 27-MAR-2003
LOCUS AX670906 Sequence 9 from Patent EP1277836.
DEFINITION AX670906
ACCESSION AX670906
VERSION AX670906.1 GI:29329409
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Korneluk,R., Mackenzie,A.E., Liston,P., Baird,S., Tsang,B. and Pratt,C.
TITLE Modulation of the iaps and naip for the treatment of proliferative diseases
JOURNAL Patent: EP 1277836-A 9 22-JAN-2003;
UNIVERSITY OF OTTAWA (CA)
LOCATION/Qualifiers
source 1. .2691
/organism="Mus musculus"
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ORIGIN
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Best Local Similarity 99.0%; Pred. No. 1e-44;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAGGAGCAGCTT 60
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QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGA 120
Db 1521 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGA 1580

QY 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGAGCCAGCATGCTAAGTGTCTAC 180
Db 1581 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGAGCCAGCATGCTAAGTGTCTAC 1640

QY 181 CCAGGGTGCAAAATACCTA 198
Db 1641 CCAGGGTGCAAAATACCTA 1658

RESULT 8
BD190871 2691 bp DNA linear PAT 17-JUL-2003
LOCUS BD190871
DEFINITION Detection and modulation of the IAPs and NAIP for the diagnosis and treatment of proliferative disease.
FEATURES
source BD190871
ACCESSION BD190871

BD190871.1 GI:33000610
JP 2002512602-A/4.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 2691)
Korneluk,R., Mackenzie,A.E., Liston,P., Baird,S., Tsang,B. and
Pratt,C.
Detection and modulation of the IAPs and NAIP for the diagnosis and
treatment of proliferative disease
Patent: JP 2002512602-A 4 23-APR-2002;
UNIVERSITY OF OTTAWA
PN JP 2002512602-A/4
PD 23-APR-2002
PF 13-FEB-1998 JP 1998531325
PR 13-FEB-1997 US 08/800929
PI ROBERT KORNELEK,ALEXANDER E MACKENZIE,PETER LISTON,STEPHEN PI
BAIRD,
PI BENJAMIN TSANG,CHRISTINE PRATT
PC A61K38/17,A61K31/70,A61K39/395,C12N15/11,C12Q1/68,G01N33/50,
PC G01N33/574,
PC A01K67/027,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATGAGTGAAGTGCCTTCCACTGTGGA 60
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QY 61 GCAAGAGCTGGATTATGCTTTAGTGAAGCGGATTAAGTGAAGTGCCTTCCACTGTGGA 120
Db 1521 GCAAGAGCTGGATTATGCTTTAGTGAAGCGGATTAAGTGAAGTGCCTTCCACTGTGGA 1580
QY 121 GGAGGCTCAGGATGGAAGCGGATTAAGTGAAGTGCCTTCCACTGTGGA 180
Db 1581 GGAGGCTCAGGATGGAAGCGGATTAAGTGAAGTGCCTTCCACTGTGGA 1640
QY 181 CCAGGCTGCAATACCTA 198
Db 1641 CCAGGCTGCAATACCTA 1658
RESULT 9
MMU88990 2691 bp mRNA linear ROD 31-MAY-1997
LOCUS
DEFINITION Mus musculus X-linked inhibitor of apoptosis (miap-3) mRNA,
complete cds.
U88990
ACCESSION U88990.1 GI:2138318
VERSION
KEYWORDS
SOURCE
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2691)
Farahani,R., Lefebvre,C., Korneluk,R.G. and MacKenzie,A.E.
Genomic Organization and Primary Characterization of miap-3: The
Murine Homologue of Human X-linked IAP
Unpublished
JOURNAL
REFERENCE 2 (bases 1 to 2691)
AUTHORS Farahani,R., Lefebvre,C., Korneluk,R.G. and MacKenzie,A.E.
TITLE Direct Submission

Submitted (07-FEB-1997) Molecular Genetics, Children's Hospital of
Eastern Ontario, 401 Smyth Rd., Ottawa, Ontario K1H 8L1, Canada
Location/Qualifiers
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/mol_type="mRNA"
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ORIGIN
Query Match 98.4%; Score 194.8; DB 10; Length 2691;
Best Local Similarity 99.0%; Pred. No. 1e-44;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 121 GGAGGCTCAGGATGGAAGCGGATTAAGTGAAGTGCCTTCCACTGTGGA 180
Db 1581 GGAGGCTCAGGATGGAAGCGGATTAAGTGAAGTGCCTTCCACTGTGGA 1640
QY 181 CCAGGCTGCAATACCTA 198
Db 1641 CCAGGCTGCAATACCTA 1658
RESULT 10
MMU36842 1988 bp mRNA linear ROD 05-JUN-1996
LOCUS
DEFINITION Mus musculus IAP homolog A (MIHA) mRNA, complete cds.

```

ACCESSION      U36842
VERSION        U36842.1  GI:1145260
KEYWORDS
SOURCE        Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS      Uren,A.G., Pakusch,M., Hawkins,C.J., Puls,K.L. and Vaux,D.L.
TITLE        Cloning and expression of apoptosis inhibitory protein homologs
              that function to inhibit apoptosis and/or bind tumor necrosis
              factor receptor-associated factors
JOURNAL       Proc. Natl. Acad. Sci. U.S.A. 93 (10), 4974-4978 (1996)
MEDLINE       96209843
PUBMED        8643514
REFERENCE
AUTHORS      Vaux,D.L., Uren,A.G. and Pakusch,M.
TITLE        Direct Submission
JOURNAL       Submitted (21-SEP-1995) M. Pakusch, The Walter and Eliza Hall
              Institute, Royal Parade, Parkville, Victoria 3050, Australia
FEATURES
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   /dev stage="6-8 weeks old"
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Matches 191; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY      1  TATGAAGCAGCGATCGTTACTTTTGGACATGGATATACTCAGTTACACAGGACGAGCTT 60
DB      1001 TATGAAGCAGCGATCGTTACTTTTGGACATGGACATCTCAGTTACACAGGACGAGCTT 1060
QY      61  GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGCCTTCCACTGTGGA 120
DB      1061 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGCCTTCCACTGTGGA 1120

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QY 121 GGAGGGCTCAGGATTCGAAGCCCAAGTGAAGACCCCTGGGACGACATGCTAGTGTAC 180
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 DB 1121 GGAGGGCTCAGGATTCGAAGCCCAAGTGAAGACCCCTGGGACGACATGCTAGTGTAC 1180
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QY 181 CCAGGGTGCAAAATACCTA 198
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 DB 1181 CCAGGGTGCAAAATACCTA 1198
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RESULT 11
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 DEFINITION Mus musculus clone RP23-396C19, DNA linear HTG 24-FEB-2003
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 ACCESSION AC109227
 VERSION AC109227.4 GI:28475838
 HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 KEYWORDS Mus musculus (house mouse)
 SOURCE
 ORGANISM
 Mus musculus
 1 (bases 1 to 205991)
 Birren,B., Nusbaum,C. and Lander,E.
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Birren,B., Nusbaum,C. and Lander,E.
 Mus musculus, clone RP23-396C19
 Unpublished
 2 (bases 1 to 205991)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
 Choepel,Y., Collangelo,M., Collins,S., Collymore,A., Cook,A.,
 Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
 Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
 Glade,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
 Kanat,A., Karatas,A., Kells,C., LaRoque,K., Lamazares,R.,
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 McSwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T.,
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 Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
 Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
 Retta,K., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
 Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
 Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Straus,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
 Topham,K., Travers,M., Travis,N., Triglio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (03-FEB-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 205991)
 Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
 Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
 Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
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 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
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 Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
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 Meldrim,J., Meneus,L., Mihova,T., Mieng,V., Murphy,T., Naylor,J.,
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 Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE
JOURNAL
COMMENT

Direct Submission
Submitted (24-FEB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 24, 2003 this sequence version replaced gi:28269624.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L20802
Center clone name: 396_C_19
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 203609 bases at least Q40
Consensus quality: 203944 bases at least Q30
Consensus quality: 204698 bases at least Q20
Insert size: 200000; agarose-1p
Insert size: 205291; sum-of-contigs
Quality coverage: 8.7 in Q20 bases; agarose-1p
Quality coverage: 8.5 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 42349: contig of 42349 bp in length
* 42350 42449: gap of 100 bp
* 42450 44657: contig of 2208 bp in length
* 44658 44757: gap of 100 bp
* 44758 51328: contig of 6571 bp in length
* 51329 51428: gap of 100 bp
* 51429 62775: contig of 11347 bp in length
* 62776 62875: gap of 100 bp
* 62876 71924: contig of 9049 bp in length
* 71925 72024: gap of 100 bp
* 72025 185178: contig of 113154 bp in length
* 185179 185278: gap of 100 bp
* 185279 203699: contig of 18421 bp in length
* 203700 203799: gap of 100 bp
* 203800 205991: contig of 2192 bp in length.
----- Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-396C19"
/clone_lib="RPCI-23 Female Mouse BAC"
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vector_side:left"
42450..44657
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44758..51328
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51429..62775
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62876..71924
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72025..185178
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185279..203699
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clone_end:17
vector_side:right"
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Best Local Similarity 96.0%; Pred. No. 2.6e-42;
Matches 190; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 TATGAACACGATCGTTACTTTTGGAAACATGATATCTCAGTTAAACAGGAGCAGCTT 60
Db 43490 TATGAACACGATCGTTACTTTTGGAAACATGATATCTCAGTTAAACAGGAGCAGCTT 43549
QY 61 GCAAGAGCTGATTTTATGCTTTAGGTGAAGGCGATAAAAGTGAAGTGCCTTCCACTGTGGA 120
Db 43550 GCAAGAGCTGATTTTATGCTTTAGGTGAAGGCGATAAAAGTGAAGTGCCTTCCACTGTGGA 43609
QY 121 GGAGGGTCCAGGATTTGGAAAGCAAGTGAAGACCCCTGGACCCAGCATCTTAAGTGTCTAC 180
Db 43610 GGAGGGTCCAGGATTTGGAAAGCAAGTGAAGACCCCTGGACCCAGCATCTTAAGTGTCTAT 43669
QY 181 CCAGGGTGCATAATACCTA 198
Db 43670 CCAGGGTGCATAATACCTA 43687

RESULT 12
AC137152/c
LOCUS
AC137152 208236 bp DNA linear HTG 27-NOV-2002
DEFINITION
Mus musculus chromosome UNK clone RP24-269A16, WORKING DRAFT
SEQUENCE, 18 unordered pieces.
AC137152
AC137152.1 GI:25054276
VERSION
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 208236)
McPherson,J.D. and Waterston,R.H.
TITLE
The sequence of Mus musculus clone
JOURNAL
Unpublished
AUTHORS
2 (bases 1 to 208236)
McPherson,J.D. and Waterston,R.H.
TITLE
Direct Submission
JOURNAL
Submitted (18-NOV-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE
3 (bases 1 to 208236)
McPherson,J.D. and Waterston,R.H.
TITLE
Direct Submission
JOURNAL
Submitted (27-NOV-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:<http://genome.wustl.edu/gsc/index.shtml>
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M.B0269A16
----- Summary Statistics -----
Sequencing vector: M13; #
Sequencing vector: plasmid; #
Chemistry: Dye-primer ET; # of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 200515 bases at least Q40
Consensus quality: 202070 bases at least Q30
Consensus quality: 203024 bases at least Q20

* NOTE: This is a 'working draft' sequence. It currently

* consists of 18 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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1 1281: contig of 1281 bp in length
* 1282 1381: gap of unknown length
* 1382 2667: contig of 1286 bp in length
* 2668 2767: gap of unknown length
* 2768 4612: contig of 1845 bp in length
* 4613 4712: gap of unknown length
* 4713 6345: contig of 1633 bp in length
* 6346 7770: gap of unknown length
* 7771 7870: gap of unknown length
* 7871 9368: contig of 1498 bp in length
* 9369 9469: gap of unknown length
* 9470 11493: contig of 2025 bp in length
* 11494 11593: gap of unknown length
* 11594 13278: contig of 1685 bp in length
* 13279 13378: gap of unknown length
* 13379 17337: contig of 3959 bp in length
* 17338 17437: gap of unknown length
* 17438 22336: contig of 5499 bp in length
* 22337 23036: gap of unknown length
* 23037 28613: contig of 5577 bp in length
* 28614 28713: gap of unknown length
* 28714 34822: contig of 6109 bp in length
* 34823 43533: gap of unknown length
* 43534 43633: gap of unknown length
* 43634 66136: contig of 22503 bp in length
* 66137 66236: gap of unknown length
* 66237 85245: contig of 19009 bp in length
* 85246 106030: gap of unknown length
* 106031 106130: gap of unknown length
* 106131 147197: contig of 41067 bp in length
* 147198 147297: gap of unknown length
* 147298 208236: contig of 60939 bp in length.
  
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FEATURES

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Best Local Similarity 96.0%; Pred.No. 2.6e-42;
Matches 190; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TATGAAGCACCGATCGTTACTTTTGGAAACATGGATATCTCAGTTAACAGGACGAGCTT 60
Db 195106 TATGAAGCACGGTCTGTTACTTTTGGAAACATGGATATCTCAGTTAACAGGACGAGCTT 195047

QY 61 GCAAGAGCTGCAATTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
Db 195046 GCAAGAGCTGCAATTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 194987

QY 121 GGAGGGCTTCAGGATTCGAAGCCAAAGTGAAGACCCCTGGGACCAGCATGCTAAAGTGCTAC 180
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QY 181 CCAGGTGCAATATACCTA 198
Db 194926 CCAGGTGCAATATACCTA 194909

RESULT 13
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LOCUS Rattus norvegicus inhibitor of apoptosis protein 3 mRNA, complete
DEFINITION
VERSION AF183429.1 GI:10765280
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM
REFERENCE
1 (bases 1 to 1491)
AUTHORS Holcik,M., Lefebvre,C.A., Hicks,K. and Korneluk,R.G.
TITLE Cloning and characterization of the rat homologues of the Inhibitor
of Apoptosis protein 1,2, and 3 genes
JOURNAL BMC Genomics 3 (1), 5 (2002)
PUBMED 11860601
REFERENCE
2 (bases 1 to 1491)
AUTHORS Holcik,M., Lefebvre,C.A., Hicks,K. and Korneluk,R.G.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-1999) Department of Biochemistry, Microbiology
and Immunology, University of Ottawa, 451 Smyth Road, Ottawa,
Ontario K1H 8M5, Canada
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ORIGIN

Query Match 91.9%; Score 182; DB 10; Length 1491;
Best Local Similarity 94.9%; Pred. No. 4.9e-41;
Matches 188; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACCTCAGTTAAACAAGGAGCAGCTT 60
DB 790 TATGACGACGAGTGGTACTTTTGGAAACATGGATATACCTCAGTTAAACAAGGAGCAGCTT 849
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGCCTTCCACTGTGGA 120
DB 850 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGCCTTCCACTGTGGA 909
QY 121 GGAGGCTCAGCGATTGGAAGCCCAAGTGAAGACCCCTGGGACGAGCATGCTAAAGTGCCTAC 180
DB 910 GGAGGCTCAGCGATTGGAAGCCCAAGTGAAGACCCCTGGGACGAGCATGCTAAAGTGCCTAT 969

RESULT 14
AF304336
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AB033366
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AB033366
AB033366.1 GI:6045147
RIAP3.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 2468)
Saito, N.
Rattus norvegicus X-linked inhibitor of apoptosis (riap3) mRNA
Published Only in Database (1999)
2 (bases 1 to 2468)
Saito, N.
Direct Submission
Submitted (07-OCT-1999) Nobuhito Saito, University of Tokyo,
Department of Neurosurgery, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-8655,
Japan (E-mail:nsaito-tky@umin.ac.jp, Tel.+81-3-5800-8853,
Fax:+81-3-5800-8655)
Location/Qualifiers
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gene

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FEATURES

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gene

CDS

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ORIGIN

Query Match 91.9%; Score 182; DB 10; Length 2468;
Best Local Similarity 94.9%; Pred. No. 4.5e-41;
Matches 188; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACCTCAGTTAAACAAGGAGCAGCTT 60
DB 1119 TATGACGACGAGTGGTACTTTTGGAAACATGGATATACCTCAGTTAAACAAGGAGCAGCTT 1178
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGCCTTCCACTGTGGA 120
DB 1179 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGCCTTCCACTGTGGA 1238
QY 121 GGAGGCTCAGCGATTGGAAGCCCAAGTGAAGACCCCTGGGACGAGCATGCTAAAGTGCCTAC 180
DB 1239 GGAGGCTCAGCGATTGGAAGCCCAAGTGAAGACCCCTGGGACGAGCATGCTAAAGTGCCTAT 1298
QY 181 CCAGGCTGCAAAATACCTA 198
DB 1299 CCAGGCTGCAAAATACCTA 1316

RESULT 15

AF304334

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

CDS

1 (bases 1 to 3032)
Lareu, R.R., Lacher, M.D., Bradley, C.K., Sridharan, R., Friis, R.R. and
Dharmarajan, A.M.
Regulated expression of inhibitor of apoptosis protein 3 in the rat
corpus luteum
Biol. Reprod. 68 (6), 2232-2240 (2003)
2 (bases 1 to 3032)
Lareu, R.R., Lacher, M., Friis, R.R. and Dharmarajan, A.M.
Direct Submission
Submitted (08-SEP-2000) Anatomy and Human Biology, University of
Western Australia, Verdum St, Nedlands, WA 6907, Australia
Location/Qualifiers
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/mol_type="mRNA"
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926. .2431
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QYINNHLTHSLGESVVRVSESVSDRNFPNSTSPNPAWAEYDAKIVTFGTWLY
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BEKLOTSGSNYSLEVLIALDLVSAQKDNSODESSQTSLOKDISTEEQLRLOEKLCK
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ORIGIN

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Best Local Similarity	94.9%	Pred. No. 4.3e-41			
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Db	1715	TATGACGCACGGATCGTTACTTTTGGAAACATGGCTATATCTCAGTTAACAGGAGCAGCTT	1774
Qy	61	GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTCTTCCACTGTGGA	120
Db	1775	GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTCTTCCACTGTGGA	1834
Qy	121	GGAGGGCTCACGGATTGGAAAGCCAAAGTGAAGACCCCTGGGACCGAGATGCTAAGTGTCTAC	180
Db	1835	GGAGGGCTCACGGATTGGAAAGCCAAAGTGAAGACCCCTGGGACCGAGATGCTAAGTGTCTAT	1894
Qy	181	CCAGGGTGCMAATACCTA	198
Db	1895	CCAGGGTGTAAATATCTA	1912

Search completed: March 13, 2004, 05:11:49
Job time : 1046.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 12, 2004, 21:10:12 ; Search time 265 Seconds
(without alignments)
3174.125 Million cell updates/sec

Title: US-09-654-743-51

Perfect score: 198

Sequence: 1 tatgaagcacgacgtgttac.....accagggcgcaataacctta 198

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: N Geneseq 26Jan04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2003as.*
- 8: Geneseqn2003bs.*
- 9: Geneseqn2003cs.*
- 10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	198	100.0	2100	2	AAT70839	Mouse apo
2	198	100.0	2100	6	ABK93872	Mouse cdn
3	194.8	98.4	2691	2	AAV55041	Murine XI
4	194.8	98.4	2691	7	ABZ58102	Mouse inh
5	186.8	94.3	1988	2	AAT72710	Mouse inh
6	173	87.4	1588	6	ABZ52803	DNA encod
7	173	87.4	1659	3	AZ48862	Human XIA
8	173	87.4	1659	7	ACA56455	Human sig
9	173	87.4	2404	6	AKK99405	DNA of AP
10	173	87.4	2540	2	AAT70836	Human apo
11	173	87.4	2540	3	AA64901	Human X-1
12	173	87.4	2540	6	ABK93869	Human cdn
13	173	87.4	2540	6	ABV94283	Breast ca
14	173	87.4	2540	7	AA153731	X-linked
15	173	87.4	2540	7	AAD49663	Human X-1
16	173	87.4	2540	8	ADB81002	RING-SH c
17	173	87.4	3000	6	ABK93875	Human cdn
18	173	87.4	5232	2	AAV55038	Human XIA
19	157	79.3	1752	4	AAD03575	Human IAP
20	149	75.3	1758	6	ABK14678	Human inh
21	149	75.3	1758	6	ABK14677	Human inh
22	149	75.3	4993	4	AAD03581	Human IAP
23	147.4	74.4	711	3	AA06940	DNA encod

24	147.4	74.4	1559	6	ABK13197	Human tes
25	147.4	74.4	1559	6	ABZ52802	DNA encod
26	145.8	73.6	711	4	AAD03582	Chimpanzee
27	144.2	72.8	711	4	AAD03583	Gorilla I
28	134.4	67.9	578	2	AAZ02960	Human IL-
29	109.6	55.4	802	2	AAZ03018	Human IL-
30	79.8	40.3	1402	2	AAZ03028	Human IL-
31	77.8	39.3	302	6	ABQ58785	Human col
32	76	38.4	2563	7	ACA56478	Human sig
33	76	38.4	2563	8	ADB80989	RING-SH c
34	76	38.4	2601	2	AAT61591	Human c-I
35	76	38.4	2666	2	AAT70837	Human apo
36	76	38.4	2676	6	ABK93870	Human cdn
37	76	38.4	3076	2	AAT72712	Human inh
38	76	38.4	3076	2	AAZ41005	Human cel
39	76	38.4	3076	2	AAZ22096	Human cel
40	76	38.4	3076	6	ABL62746	Breast ca
41	76	38.4	3076	6	ABL66325	Lung canc
42	76	38.4	3076	7	ABX10968	cDNA enco
43	76	38.4	3076	9	AAD60472	Human cel
44	76	38.4	3153	7	ABZ58104	Inhibitor
45	76	38.4	3164	7	ABV75363	Human CIA

ALIGNMENTS

RESULT 1
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ID AAT70839 standard; cdna; 2100 BP.
XX
AC AAT70839;
XX
DT 02-SEP-1997 (first entry)
XX Mouse apoptosis inhibitor m-xiap cdna.
XX
DE
XX
KW Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; M-XIAP;
KW HIV; AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia;
KW myocardial infarction; stroke; reperfusion injury;
KW toxin-induced liver disease; gene therapy; diagnosis; ds.
XX
OS Mus sp.
XX
FH Key
CDS Location/Qualifiers
FT 127..1617
FT /*tag= a
XX
XX WO9706255-A2.
XX
XX PD 20-FEB-1997.
XX
XX ABK93872 Mouse cdn
XX AAV55041 Murine XI
XX ABZ58102 Mouse inh
XX AAT72710 Mouse inh
XX PR 04-AUG-1995; 95US-00511485.
XX PR 22-DEC-1995; 95US-00576956.
XX
XX AAZ48862 Human XIA
XX ACA56455 Human sig
XX AAK99405 DNA of AP
XX AAT70836 Human apo
XX AAG4901 Human X-1
XX DR ABK93869 Human cdn
XX ABV94283 Breast ca
XX AA153731 X-linked
XX AAD49663 Human X-1
XX ADB81002 RING-SH c
XX ABK93875 Human cdn
XX AAV55038 Human XIA
XX AAD03575 Human IAP
XX ABK14678 Human inh
XX ABK14677 Human inh
XX AAD03581 Human IAP
XX AA06940 DNA encod

Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of susceptibility to apoptotic disease.
Claim 11; Page 78-79; 219pp; English.
Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and hiap-2 genes (AAT70836-41) respectively code for a new class of mammalian proteins (AAW19581-86) that are inhibitors of apoptosis (IAP). The murine

CC xiap gene (for X-linked IAP gene) sequence was constructed from 12
 CC overlapping clones isolated from a mouse embryo lambda-gt10 cDNA library
 CC and from a mouse FIX II genomic library using human xiap cDNA as probe.
 CC IAP nucleic acids can be used to express IAP polypeptides in cells and
 CC animals to inhibit apoptosis, and as primers and probes to identify and
 CC isolate additional IAP genes, as well as in methods for treating diseases
 CC and disorders involving apoptosis (anti-apoptotic gene therapy).
 XX
 SQ Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 U; 0 Other;
 Query Match 100.0%; Score 198; DB 2; Length 2100;
 Best Local Similarity 100.0%; Pred. No. 2e-58;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TATGAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTTAAAGGAGCAGCTT 60
 Db 916 TATGAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTTAAAGGAGCAGCTT 975
 QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
 Db 976 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 1035
 QY 121 GGAGGCTCACGATGGAGCCAGTGAAGCCAGTGAAGCCCTGGGACCGATGCTTAAGTGTCTAC 180
 Db 1036 GGAGGCTCACGATGGAGCCAGTGAAGCCAGTGAAGCCCTGGGACCGATGCTTAAGTGTCTAC 1095
 QY 181 CCAGGCTGCAATACCTA 198
 Db 1096 CCAGGCTGCAATACCTA 1113
 RESULT 2
 ABK93872
 ID ABK93872 standard; cDNA; 2100 BP.
 AC ABK93872;
 XX
 DT 26-AUG-2002 (first entry)
 DE Mouse cDNA encoding inhibitor of apoptosis, XIAP.
 XX
 KW Mouse; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
 KW cytotatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.
 XX
 OS Mus sp.
 XX
 PN WO200226968-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 27-SEP-2001; 2001WO-CA001379.
 XX
 PR 28-SEP-2000; 2000US-00672717.
 XX
 XX (UYOT-) UNIV OTTAWA.
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
 XX WPI; 2002-479562/51.
 XX P-PSDB; ABG65665.
 DR
 XX Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
 PT apoptosis in a cell, for treating cancer and other proliferative
 PT diseases.
 PT
 XX Disclosure; Fig 4; 135pp; English.
 PS
 XX The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC

CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse or
 CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer), and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a mouse IAP
 CC cDNA sequence
 XX
 SQ Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 U; 0 Other;
 Query Match 100.0%; Score 198; DB 6; Length 2100;
 Best Local Similarity 100.0%; Pred. No. 2e-58;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TATGAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTTAAAGGAGCAGCTT 60
 Db 916 TATGAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTTAAAGGAGCAGCTT 975
 QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
 Db 976 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 1035
 QY 121 GGAGGCTCACGATGGAGCCAGTGAAGCCAGTGAAGCCCTGGGACCGATGCTTAAGTGTCTAC 180
 Db 1036 GGAGGCTCACGATGGAGCCAGTGAAGCCAGTGAAGCCCTGGGACCGATGCTTAAGTGTCTAC 1095
 QY 181 CCAGGCTGCAATACCTA 198
 Db 1096 CCAGGCTGCAATACCTA 1113
 RESULT 3
 AAV55041
 ID AAV55041 standard; cDNA; 2691 BP.
 AC AAV55041;
 XX
 DT 13-NOV-1998 (first entry)
 DE Murine XIAP coding sequence.
 XX
 KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
 KW proliferative disease; IAP; therapy; cancer; mouse; XIAP protein; ss.
 XX
 OS Mus sp.
 XX
 XX Key Location/Qualifiers
 FH 672..2162
 FT CDS /*tag= a
 FT /product= "XIAP"
 FT
 XX
 PN WO9835693-A2.
 XX
 XX 20-AUG-1998.
 XX
 XX 13-FEB-1998; 98WO-IB000781.
 PF
 XX 13-FEB-1997; 97US-00800929.
 PR
 XX (UYOT-) UNIV OTTAWA.
 PA
 XX Korneluk R, Mackenzie AE, Liston P, Baird S, Tsang B, Pratt C;
 XX
 XX

DR WPI; 1998-467164/40.
DR P-PSDB; AAW69297.

XX Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
XX or NAIP polypeptide - also methods for prognosis based on presence of IAP
PT and NAIP, specifically applied to cancers involving p53 mutations.
XX

XX Claim 13; Fig 4; 147pp; English.

PS This sequence encodes the mouse XIAP protein, which is an inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, especially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors

XX Sequence 2691 BP; 819 A; 479 C; 562 G; 831 T; 0 U; 0 Other;

Query Match 98.4%; Score 194.8; DB 2; Length 2691;

Best Local Similarity 99.0%; Pred. No. 2.8e-57;

Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGATATCTCAGTTAACAGGAGCAGCTT 60
DB 1461 TATGAAGCAGCGATCGTTACTTTTGGACATGATATCTCAGTTAACAGGAGCAGCTT 1520

QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCGATAAAGTGAAGTCTTCCACTGTGA 120
DB 1521 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCGATAAAGTGAAGTCTTCCACTGTGA 1580

QY 121 GGAGGGCTCAGCGATTGGAGCCAAAGTGAAGACCCCTGGACACGATGCTAAGTGTCTAC 180
DB 1581 GGAGGGCTCAGCGATTGGAGCCAAAGTGAAGACCCCTGGACACGATGCTAAGTGTCTAC 1640

QY 181 CCAGGGTGCAAAATACCTA 198

DB 1641 CCAGGGTGCAAAATACCTA 1658

RESULT 4

ID ABZ58102 standard; cDNA; 2691 BP.

XX ABZ58102;

XX 22-APR-2003 (first entry)

DE Mouse inhibitor of apoptosis protein MIAP3 cDNA.

XX Inhibitor of apoptosis; MIAP3; mouse; apoptosis; cancer; leukaemia;
KW lymphoma; neuroblastoma; carcinoma; melanoma; cytostatic; gene therapy;
KW gene; ss.

XX Mus sp.

OS Location/Qualifiers

672..2162

/*tag= a

/*product= "MIAP3"

WO2003004606-A2.

XX 16-JAN-2003.

XX

PF 03-JUL-2002; 2002WO-US021002.

XX 03-JUL-2001; 2001US-00898158.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Troy CM, Shelanski ML;

XX WPI; 2003-210351/20.

XX P-PSDB; ABP72157.

XX New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for

XX treating cancer, neurodegenerative disorder or cardiomyopathy.

XX Disclosure; Fig 15B; 124pp; English.

XX The present sequence is that of cDNA encoding murine inhibitor of

XX apoptosis protein MIAP3. The invention provides a nucleic acid, such as

XX an antisense oligonucleotide, which specifically hybridizes to a nucleic

XX acid encoding an inhibitor of apoptosis protein, especially MIAP1, MIAP2,

XX MIAP3, CIAPI, CIAPI2 and XIAP. A claimed method for inducing a cell's

XX death comprises contacting the cell with the nucleic acid under

XX conditions permitting the nucleic acid to enter the cell, especially the

XX use of a vector, liposome, or a mechanical or electrical means. The

XX method is used to treat acute lymphocytic leukaemia, acute myelogenous

XX leukaemia, lung cancer, breast cancer, ovarian cancer, prostate cancer,

XX lymphoma, Hodgkin's disease, malignant melanoma, neuroblastoma, renal

XX cell carcinoma and squamous cell carcinoma (all claimed)

XX Sequence 2691 BP; 819 A; 479 C; 562 G; 831 T; 0 U; 0 Other;

Query Match 98.4%; Score 194.8; DB 7; Length 2691;

Best Local Similarity 99.0%; Pred. No. 2.8e-57;

Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGATATCTCAGTTAACAGGAGCAGCTT 60
DB 1461 TATGAAGCAGCGATCGTTACTTTTGGACATGATATCTCAGTTAACAGGAGCAGCTT 1520

QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCGATAAAGTGAAGTCTTCCACTGTGA 120
DB 1521 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCGATAAAGTGAAGTCTTCCACTGTGA 1580

QY 121 GGAGGGCTCAGCGATTGGAGCCAAAGTGAAGACCCCTGGACACGATGCTAAGTGTCTAC 180
DB 1581 GGAGGGCTCAGCGATTGGAGCCAAAGTGAAGACCCCTGGACACGATGCTAAGTGTCTAC 1640

QY 181 CCAGGGTGCAAAATACCTA 198

DB 1641 CCAGGGTGCAAAATACCTA 1658

RESULT 5

ID AAT72710

XX AAT72710 standard; DNA; 1988 BP.

XX AAT72710;

XX 16-SEP-1997 (first entry)

DE Mouse inhibitor of apoptosis protein homologue MIHA DNA.

XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA;

XX degenerative disease; infectious disease; autoimmune disease; cancer;

XX gene therapy; diagnosis; ss.

XX Mus musculus.

OS Location/Qualifiers

212..1702

/*tag= a

WO9723501-A1.

XX Key

XX CDS

XX

XX

XX

XX

XX

XX

XX

```
XX PD 03-JUL-1997.
XX PF 20-DEC-1996; 96WO-AU000827.
XX PR 22-DEC-1995; 95AU-00007275.
XX PA (AMBA-) AMRAD OPERATIONS PTY LTD.
XX PI Vaux DL;
XX DR WPI; 1997-350966/32.
XX DR P-PSDB; AAW19745.
XX PT Isolated protein homologues of viral inhibitors of apoptosis - used to
XX PT modulate apoptosis for treatment of degenerative, infectious or
XX PT auto-immune diseases and cancer.
XX PS Claim 24; Page 44-47; 136pp; English.
XX CC An isolated nucleic acid molecule (AAT72710) codes for mammalian IAP
XX CC homologue A (MIHA) (AAW19745), a murine homologue of baculovirus
XX CC inhibitor of apoptosis protein (IAP). It was isolated from a mouse liver
XX CC cDNA library on the basis of homology to Oryza pseudotsuguta
XX CC polyhedrosis virus IAP BIR and RING finger amino acid motifs. Animal IAP
XX CC homologue nucleic acids (see also AAT72711-17) can be used to produce
XX CC polypeptides useful in methods for modulating apoptosis in animal cells,
XX CC specifically for treatment, by inhibition, of degenerative and infectious
XX CC disease or, by promotion, of cancer and autoimmune disease, and can be
XX CC used for gene therapy of these diseases
XX SQ Sequence 1988 BP; 605 A; 367 C; 459 G; 557 T; 0 U; 0 Other;
Query Match 94.3%; Score 186.8; DB 2; Length 1988;
Best Local Similarity 96.5%; Pred. No. 1.6e-54;
Matches 191; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGATATCTACGTTCAGTTACAGGAGGAGCTT 60
DB 1001 TATGAAGCAGCGATCGTTACTTTTGGACATGATGACATCCCTCAGTTACAGGAGGAGCTT 1060
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATTAAGTGAAGTCTTCCACTGTGGA 120
DB 1061 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATTAAGTGAAGTCTTCCACTGTGGA 1120
QY 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGGACGACGATGCTAAGTCTTAC 180
DB 1121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGGACGACGATGCTAAGTCTTAC 1180
QY 181 CCAGGGTGCAAAATACCTA 198
DB 1181 CCAGGGTGCAAAATACCTA 1198
RESULT 6
ABS52803
ID ABS52803 standard; DNA; 1588 BP.
XX AC ABS52803;
XX DT 15-NOV-2002 (first entry)
XX DE DNA encoding X-linked inhibitor of apoptosis, XIAP.
XX KW Inhibitor of apoptosis protein; IAP; testis; XIAP; apoptosis; TIAP;
XX KW fertility; testicular cancer; male infertility; male birth control;
XX KW X-linked inhibitor of apoptosis; gene; ds.
XX OS Mammalia.
XX FH Key
XX FT CDS
XX FT Location/Qualifiers
XX FT 34..1527
XX FT /*tag= a
```

```
/transl except= (pos:34..36, aa:Xaa)
/product= "X-linked inhibitor of apoptosis protein, XIAP"
/partial
/notes= "Start codon illegible in specification;
represented as nnn"
US2002086409-A1.
04-JUL-2002.
18-DEC-2001; 2001US-00024433.
29-JAN-1998; 98US-0073001P.
29-JAN-1999; 99US-00239867.
(KORN/) KORNELUK R G.
(LAGA/) LAGACE M.
Korneluk RG, Lagace M;
WPI; 2002-642245/69.
P-PSDB; ABG32418.
Novel polypeptide, a member of inhibitor of apoptosis family of proteins
that is expressed in testes useful for modulating apoptosis in cells,
particular cells involved in male fertility.
Example 3; Fig 4A; 24pp; English.
A substantially pure TIAP polypeptide (I), a member of IAP (inhibitor of
apoptosis) family of proteins that is expressed in the testes. (I) is
useful for identifying a compound that modulates TIAP biological activity
(I) is useful for increasing apoptosis in a cell, preferably a germ-line
cell and for increasing fertility in an animal. (I) is useful for
treating or preventing apoptosis which occurs as a part of testicular
cancer and male infertility. TIAP may be manipulated for use as a male
birth control. TIAP polypeptides and nucleic acid sequences also have
diagnostic use in the detection or monitoring of conditions involving
aberrant levels of apoptosis. The present sequence represents the coding
sequence of X-linked inhibitor of apoptosis (XIAP)
Sequence 1588 BP; 505 A; 274 C; 359 G; 444 T; 0 U; 6 Other;
Query Match 87.4%; Score 173; DB 6; Length 1588;
Best Local Similarity 92.4%; Pred. No. 9.4e-50;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAAGCAGGATCGTTACTTTTGGACATGATATCTCAGTTAACAGGAGGAGCTT 60
DB 826 TATGAAGCAGGATCGTTACTTTTGGACATGATATCTCAGTTAACAGGAGGAGCTT 885
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATTAAGTGAAGTCTTCCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATTAAGTGAAGTCTTCCACTGTGGA 945
QY 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGGACGACGATGCTAAGTCTTAC 180
DB 946 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGGACGACGATGCTAAGTCTTAC 1005
QY 181 CCAGGGTGCAAAATACCT 197
DB 1006 CCAGGGTGCAAAATATCT 1022
RESULT 7
AAZ48862
ID AAZ48862 standard; cDNA; 1659 BP.
XX AC AAZ48862;
XX DT 24-MAR-2000 (first entry)
XX DE Human XIAP coding sequence.
```

XX Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
KW transforming growth factor-beta activated kinase 1; monocyte migration;
KW TAK1 binding protein 1; extracellular matrix protein production;
KW cell growth inhibitor; beta-amyloid protein deposition;
KW immunosuppression; Transforming growth factor-beta; ds.
XX
OS Homo sapiens.
XX
PN JPI1326328-A.
XX
PD 26-NOV-1999.
XX
PF 13-MAY-1998; 98JP-00130378.
XX
PR 13-MAY-1998; 98JP-00130378.
XX
PA (MATS/) MATSUMOTO K.
XX
XX WPI; 2000-078337/07.
DR P-PSDB; AAY59451.
XX
PT Screening a substance which inhibits combination of the X-linked
PT inhibitor of apoptosis protein.
XX
PS Disclosure; Page 28-30; 43pp; Japanese.
XX
CC This sequence encodes the human XIAP protein. The invention relates to a
CC method for screening a substance inhibiting the formation of a complex
CC between XIAP and TAB1, in which X-linked inhibitor of apoptosis protein
CC (XIAP), transforming growth factor-beta activated kinase 1(TAK1) binding
CC protein 1(TAB1) and a substance to be tested are contacted with each
CC other and then the presence or formation of a complex between XIAP and
CC TAB1 is detected. The substance can be used as a drug for extracellular
CC matrix protein production enhancement, cell growth inhibition, monocyte
CC migration, physiologically active substance induction, immunosuppression,
CC and beta-amyloid protein deposition. A substance inhibiting the formation
CC of a complex between TAB1 and XIAP as well as between XIAP and TGF-beta
CC (transforming growth factor-beta) type I and/or type II receptor is
CC useful as a drug
XX
SQ Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 U; 0 Other;
Query Match 87.4%; Score 173; DB 3; Length 1659;
Best Local Similarity 92.4%; Pred. No. 9.6e-50;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTACTCAGTTAACAGGAGCAGCTT 60
DB 874 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTACTCAGTTAACAGGAGCAGCTT 933
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGATAAAGTGAAGTCTTCCACTGTGGA 120
DB 934 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGATAAAGTGAAGTCTTCCACTGTGGA 993
QY 121 GGAGGGCTCAGGATCGGATTTGGAAAGTGAAGCCCTTGGGACAGCATGCTAAAGTCTAC 180
DB 994 GGAGGGCTAACTGATTTGGAAAGCCAGTGAAGCCCTTGGGACAGCATGCTAAAGTCTAT 1053
QY 181 CCAGGGTGCATACCT 197
DB 1054 CCAGGGTGCATATCT 1070
RESULT 8
ID ACA56455
XX ACA56455 standard; cDNA; 1659 BP.
AC ACA56455;
XX
XX 06-JUN-2003 (first entry)
XX
DE Human signalling pathway polynucleotide probe SEQ ID NO 1053.

XX Human; probe; ss; array element; Parkinson's disease;
KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
XX immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
OS Homo sapiens.
XX
PN US6500938-B1.
XX
PD 31-DEC-2002.
XX
PF 30-JAN-1998; 98US-00016434.
XX
PR 30-JAN-1998; 98US-00016434.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
XX Au-Young J, Seilhamer JJ;
XX WPI; 2003-352189/33.
XX
PT Combination of polynucleotide probes, useful as array elements in a
PT microarray for monitoring the expression of a number of target
PT polynucleotides.
XX
PS Claim 1; SEQ ID NO 1053; 65pp; English.
XX
CC The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format directly from USPIO at
CC seqdata.uspto.gov/sequence.html?DocID=06500938B1
XX
SQ Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 U; 0 Other;
Query Match 87.4%; Score 173; DB 7; Length 1659;
Best Local Similarity 92.4%; Pred. No. 9.6e-50;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCGTTACTTTTGGAAAGTGAAGTGAAGTCTTCCACTGTGGA 60
DB 874 TATGAAGCAGCGATCGTTACTTTTGGAAAGTGAAGTGAAGTCTTCCACTGTGGA 933
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGATAAAGTGAAGTCTTCCACTGTGGA 120
DB 934 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGATAAAGTGAAGTCTTCCACTGTGGA 993
QY 121 GGAGGGCTCAGGATTTGGAAAGTGAAGCCCTTGGGACAGCATGCTAAAGTCTAC 180
DB 994 GGAGGGCTAACTGATTTGGAAAGCCAGTGAAGCCCTTGGGACAGCATGCTAAAGTCTAT 1053
QY 181 CCAGGGTGCATACCT 197
DB 1054 CCAGGGTGCATATCT 1070

RESULT 9
AAK99405
ID AAK99405 standard; DNA; 2404 BP.
XX
AC AAK99405;
XX
DT 27-JUN-2002 (first entry)
XX
DE DNA of APP related human homologue hCP35211.
XX
KW Neuroprotective; neurotropic; transgenic fly; Alzheimer's disease; Abeta;
KW amyloid precursor protein; tissue-specific expression control; human APP;
KW APP pathway modulator; gene therapy; gene; ds.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 692..1528
FT /*tag= a
FT /product= "Protein of human homologue hCP35211"
FT /note= "No start codon"
XX
PN W0200226820-A2.
XX
PD 04-APR-2002.
XX
PF 01-OCT-2001; 2001WO-EP011345.
XX
PR 29-SEP-2000; 2000US-0236893P.
PR 14-JUN-2001; 2001US-0298309P.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;
PI Reinhardt MWH, Zusman S;
XX
DR WPI; 2002-315796/35.
DR P-PSDB; AAC20511.
XX
PT New transgenic fly, containing DNA encoding an Abeta portion of human
PT APP, useful for identifying agents which modulate the APP pathway and
PT which can be used to treat Alzheimer's disease.
PS Example 4; Page 111; 129pp; English.
XX
CC The invention relates to a transgenic fly whose genome comprises DNA
CC encoding a polypeptide having the Abeta portion of human amyloid
CC precursor protein (APP), fused to a signal sequence. The DNA sequence
CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
CC the specification. The DNA sequence is operably linked to a tissue-
CC specific expression control sequence. Expression of the sequence gives
CC the fly an altered phenotype. The purpose of the invention is for
CC identifying agents that inhibit or promote the expression and/or function
CC of genes or encoded polypeptides which modify the APP pathway. The agent
CC is a compound, triple helix DNA, antisense oligonucleotide, double
CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used
CC to treat conditions such as Alzheimer's disease. The agent can be used as
CC an APP pathway modulator or in gene therapy. This polynucleotide sequence
CC represents the DNA of the APP related human homologue hCP35211
XX
SQ Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 U; 0 Other;
Query Match 87.4%; Score 173; DB 6; Length 2404;
Best Local Similarity 92.4%; Pred. No. 1.1e-49;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGGAGCGCTT 60
DB 827 TATGAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGGAGCGCTT 886
QY 61 GCAAGAGCTGGATTTATGCTTTAGCTTAAAGTGAAGCGATAAAGTGAAGTCTCCACTGTGGA 120
|||||

DB 887 GCAAGAGCTGGATTTATGCTTTAGCTTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 946
QY 121 GGAGGGCTCAGGATTCGAGCCCAAGTGAAGCCCTGGGACGACATCTAAGTGTAC 180
DB 947 GGAGGGCTAACTGATTTGGAAGCCCAAGTGAAGCCCTGGGACACATCTAAGTGTAT 1006
QY 181 CCAGGGTGCAAAATACCT 197
DB 1007 CCAGGGTGCAAAATATCT 1023
RESULT 10
AAT70836
ID AAT70836 standard; cDNA; 2540 BP.
XX
AC AAT70836;
XX
DT 02-SEP-1997 (first entry)
XX
DE Human apoptosis inhibitor xiap cDNA.
XX
KW Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; XIAP; HIV;
KW AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia;
KW myocardial infarction; stroke; reperfusion injury;
KW toxin-induced liver disease; gene therapy; diagnosis; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 34..1527
FT /*tag= a
XX
PN W09706255-A2.
XX
PD 20-FEB-1997.
XX
PF 05-AUG-1996; 96WO-IB001022.
XX
PR 04-AUG-1995; 95US-00511485.
PR 22-DEC-1995; 95US-00576956.
XX
PA (UVOY-) UNIV OTTAWA.
XX
PI Korneluk RG, Mackenzie AB, Baird S, Liston P;
XX
DR WPI; 1997-154262/14.
DR P-PSDB; AAW19581.
XX
PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
PT inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of
PT susceptibility to apoptotic disease.
XX
PS Claim 12; Page 67-68; 219pp; English.
XX
CC Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and hiap-2
CC genes (AA70836-41) respectively code for a new class of mammalian
CC proteins (AAW19581-86) that are inhibitors of apoptosis (IAP). The xiap
CC gene (for X-linked IAP gene) was isolated from a human foetal brain Zap1
CC cDNA library using an X-linked sequence tag site that shows strong
CC homology with the conserved ring zinc finger domain of baculovirus CpiAP
CC and OpIAP genes. The gene was assigned to chromosome Xq25 by FISH. IAP
CC nucleic acids can be used to express IAP polypeptides in cells and
CC animals to inhibit apoptosis, and as primers and probes to identify and
CC isolate additional IAP genes, as well as in methods for treating diseases
CC and disorders involving apoptosis (anti-apoptotic gene therapy)
XX
SQ Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 0 U; 1 Other;
Query Match 87.4%; Score 173; DB 2; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.1e-49;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGGAGCGCTT 60
|||||

Db 826 TATGAGACCGATCTTTACTTTTGGACATGGATATCTCAGTTTACAGGAGCAGCTT 885
 Qy 61 GCAAGAGCTGGATTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
 Db 886 GCAAGAGCTGGATTTATGCTTTTAGTGAAGTGAAGTGAAGTCTTCCACTGTGGA 945
 Qy 121 GGAGGGCTCACGATTTGGAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGTCTAC 180
 Db 946 GGAGGGCTCACTGATTTGAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGTCTAC 1005
 Qy 181 CCAGGGTGCAATACCT 197
 Db 1006 CCAGGGTGCAATATCT 1022
 RESULT 11
 AA64901
 ID AAA64901 standard; DNA; 2540 BP.
 AC AAA64901;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Human X-linked inhibitor of apoptosis DNA.
 XX
 KW X-linked inhibitor of apoptosis; XIAP; hILP; MIHA; U45880; antisense;
 KW antinflammatory; cytostatic; tumour; ds.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 34..1527
 FT /*tag= a
 FT /product= "X-linked inhibitor of apoptosis"
 XX
 PN US0807173-A.
 XX
 PD 11-JUL-2000.
 XX
 PF 09-SEP-1999; 99US-00392580.
 XX
 PR 09-SEP-1999; 99US-00392580.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Cowser LM, Ackermann EJ;
 XX
 DR WPI; 2000-498201/44.
 DR P-PSDB; AAY99985.
 XX
 PT Antisense compound useful for research reagents, diagnostics, prophylaxis
 PT and for treating disorders associated with X-linked inhibitor of
 PT apoptosis, modulates expression of X-linked inhibitor of apoptosis.
 PS Example 13; Col 43-48; 33pp; English.
 XX
 CC The present invention relates to antisense oligonucleotides designed to
 CC inhibit expression of the human X-linked inhibitor of apoptosis. The
 CC present sequence is the X-linked inhibitor of apoptosis DNA. Modified
 CC phosphorothioate 2'-methoxyethyl (2'-MOE) oligonucleotides are more
 CC effective inhibitors than unmodified oligonucleotides. The
 CC oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis
 CC expression in cells and tissues in vitro. The oligonucleotides are also
 CC useful for treating animals or humans, prone to a disease associated with
 CC X-linked inhibitor of apoptosis. The oligonucleotides may also be used
 CC prophylactically to prevent infection, inflammation or tumour formation
 XX
 SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;
 Query Match 87.4%; Score 173; DB 3; Length 2540;
 Best Local Similarity 92.4%; Pred. No. 1.1e-49;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TATGAGACCGATCTTTACTTTTGGACATGGATATCTCAGTTTACAGGAGCAGCTT 60
 Db 826 TATGAGACCGATCTTTACTTTTGGACATGGATATCTCAGTTTACAGGAGCAGCTT 885
 Qy 61 GCAAGAGCTGGATTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
 Db 886 GCAAGAGCTGGATTTATGCTTTTAGTGAAGTGAAGTGAAGTCTTCCACTGTGGA 945
 Qy 121 GGAGGGCTCACGATTTGGAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGTCTAC 180
 Db 946 GGAGGGCTCACTGATTTGAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGTCTAC 1005
 Qy 181 CCAGGGTGCAATACCT 197
 Db 1006 CCAGGGTGCAATATCT 1022
 RESULT 12
 ABK93869
 ID ABK93869 standard; cDNA; 2540 BP.
 AC ABK93869;
 XX
 DT 26-AUG-2002 (first entry)
 XX
 DE Human cDNA encoding inhibitor of apoptosis, XIAP #1.
 XX
 KW Human; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
 KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200226968-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 27-SEP-2001; 2001WO-CA001379.
 XX
 PR 28-SEP-2000; 2000US-00672717.
 XX
 PA (UYOT-) UNIV OTTAWA.
 PA (ABGE-) AEGERA THERAPEUTICS INC.
 XX
 PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
 XX
 DR WPI; 2002-479562/51.
 DR P-PSDB; ABG65663.
 XX
 PT Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
 PT apoptosis in a cell, for treating cancer and other proliferative
 PT diseases.
 PS Disclosure; Fig 1; 135pp; English.
 XX
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (1) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse or
 CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic

CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a human IAP
CC cDNA sequence
XX
SQ Sequence 2540 BP; 782 A; 415 C; 549 G; 772 T; 0 U; 22 Other;
Query Match 87.4%; Score 173; DB 6; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.1e-49;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTTAAAGGAGCGAGCTT 60
DB 826 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTTAAAGGAGCGAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 945
QY 121 GGAGGGCTCAGGATTCGAAAGCCAGTGAAGACCCCTGGGACCATGCTTAAAGTGTCTAC 180
DB 946 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 945
QY 181 CCAGGCTGCAATACCT 197
DB 1006 CCAGGCTGCAATATCT 1022
RESULT 13
ABV94283
ID ABV94283 standard; cDNA; 2540 BP.
AC ABV94283;
XX
XX
DT 08-JAN-2003 (first entry)
XX
DE Breast carcinoma related nucleotide sequence SEQ ID NO:274.
XX
XX Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;
XX ss.
XX Homo sapiens.
XX
FN WO200246467-A2.
XX
XX
PD 13-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-IB002811.
PF
XX 08-DEC-2000; 2000US-0254090P.
PR
XX 07-DEC-2001; 2001US-00007926.
PR
XX (IPSO-) IPSOGEN.
PA
XX Bertucci F, Houlgatte R, Birnbaum D, Nguyen C, Viens P, Fert V;
XX
PI WPI; 2002-619023/66.
XX
XX Novel polynucleotide library useful in molecular characterization of a
PT carcinoma, comprising a pool of polynucleotide sequences or its
PT subsequences which are either underexpressed or overexpressed in tumor
PT cells.
XX
XX Claim 1; Page 289; 401pp; English.
PS
XX The present invention describes a polynucleotide library (I) useful in
CC the molecular characterisation of a carcinoma, comprising a pool of
CC polynucleotides or its subsequences which are either underexpressed or
CC overexpressed in tumor cells, and correspond to any of the
CC polynucleotide sequences chosen from the 468 sequences given in ABV94010
CC to ABV94477. Also described: (1) a polynucleotide array (II) useful for
CC the prognosis or diagnostic of tumour, comprising (I); and (2) detecting
CC (M1) differentially expressed polynucleotide sequences which are

CC correlated with a cancer, involves obtaining a polynucleotide sample from
CC a patient, and reacting the polynucleotide sample obtained with a probe
CC immobilised on a solid support, where the probe comprises any combination
CC of the polynucleotide sequences of (I) or its expression products encoded
CC by polynucleotide sequences of (I), and detecting the reaction product.
CC (I) have cytostatic activities and can be used as anti-tumour agents. (I)
CC is useful in molecular characterisation of a carcinoma. (I) and (II) are
CC useful for the prognosis or diagnostic of tumour, in differentiating a
CC normal cell from a cancer cell, detecting a hormone sensitive tumour
CC cell, differentiating a tumour with lymph nodes from a tumour without
CC lymph nodes, differentiating antracycline-sensitive tumours from
CC antracycline-insensitive tumours, and classifying good and poor prognosis
CC primary breast tumours. (I) is useful for large-scale molecular
CC characterisation of breast cancer that help in prediction, prognosis and
CC cancer treatment, and for detecting differentially expressed genes that
CC correlated with a cancer
XX
SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;
Query Match 87.4%; Score 173; DB 6; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.1e-49;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTTAAAGGAGCGAGCTT 60
DB 826 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTTAAAGGAGCGAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 945
QY 121 GGAGGGCTCAGGATTCGAAAGCCAGTGAAGACCCCTGGGACCATGCTTAAAGTGTCTAC 180
DB 946 GGAGGGCTTAACTGATTTGGAGCCAGTGAAGACCCCTTGGGACACATGCTTAAAGTGTAT 1005
QY 181 CCAGGCTGCAATACCT 197
DB 1006 CCAGGCTGCAATATCT 1022
RESULT 14
AAL53731
ID AAL53731 standard; RNA; 2540 BP.
XX
XX AAL53731;
XX
DT 07-FEB-2003 (first entry)
XX
XX X-linked inhibitor of apoptosis protein SEQ ID NO 25.
DE
XX Target RNA; target RNA:support-attached test compound; flow cytometry;
KW mass spectrometry; high-throughput screening; RNA motif; ss.
XX
XX Homo sapiens.
OS
XX WO200283837-A1.
PN
XX 24-OCT-2002.
PD
XX 11-APR-2002; 2002WO-US011758.
PF
XX 11-APR-2001; 2001US-0282966P.
PR
XX (PTCT-) PTC THERAPEUTICS INC.
XX
XX Almstead NG;
PI
XX WPI; 2003-075534/07.
DR
XX Identifying a test compound that binds to a target RNA molecule by
PT separating the detectably labeled target RNA:support-attached test
PT compound complex from uncomplexed target RNA molecules and test compounds
PT by flow cytometry.

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OM nucleic - nucleic search, using sw model

Run on: March 13, 2004, 04:07:08 ; Search time 62 Seconds
(without alignments)
1772.263 Million cell updates/sec

Title: US-09-654-743-51

Perfect score: 198

Sequence: 1 tatgaagcagcgatcggttac.....accaggtgcaaatacctta 198

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq: *
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	198	100.0	2100	2	US-08-511-485-9
2	198	100.0	2100	4	US-09-201-936-9
3	198	100.0	2100	4	US-09-011-356-9
4	198	100.0	2100	4	US-09-672-717-224
5	194.8	98.4	2691	3	US-09-212-971-9
6	194.8	98.4	2691	3	US-08-800-929A-9
7	194.8	98.4	2691	4	US-09-617-053A-9
8	173	87.4	1588	4	US-09-233-867-3
9	173	87.4	1659	4	US-09-016-434-1053
10	173	87.4	2540	2	US-08-511-485-3
11	173	87.4	2540	3	US-09-392-580-1
12	173	87.4	2540	4	US-09-201-936-3
13	173	87.4	2540	4	US-09-023-655-900
14	173	87.4	2540	4	US-09-011-356-3
15	173	87.4	2540	4	US-09-672-717-218
16	173	87.4	3000	4	US-09-672-717-231
17	173	87.4	5232	3	US-09-212-971-3
18	173	87.4	5232	3	US-08-800-929A-3
19	173	87.4	5232	4	US-09-617-053A-3
20	147.4	74.4	711	3	US-09-121-979-3
21	147.4	74.4	711	3	US-09-332-319-3
22	147.4	74.4	1559	4	US-09-233-867-1
23	134.4	67.9	152331	3	US-09-128-155-16
24	109.6	55.4	176373	3	US-09-128-155-17
25	76	38.4	2563	4	US-09-016-434-1076
26	76	38.4	2563	4	US-09-023-655-894
27	76	38.4	2601	3	US-08-569-749-3

28 76 38.4 2601 5 PCT-US96-12860-3 Sequence 3, Appli
29 76 38.4 2676 2 US-08-511-485-5 Sequence 5, Appli
30 76 38.4 2676 4 US-09-201-936-5 Sequence 5, Appli
31 76 38.4 2676 4 US-09-011-356-5 Sequence 5, Appli
32 76 38.4 2676 4 US-09-672-717-220 Sequence 220, App
33 76 38.4 3076 2 US-09-205-144-1 Sequence 1, Appli
34 76 38.4 6669 3 US-09-212-971-5 Sequence 5, Appli
35 76 38.4 6669 3 US-08-800-929A-5 Sequence 5, Appli
36 76 38.4 6669 4 US-09-617-053A-5 Sequence 5, Appli
37 76 38.4 6669 4 US-09-672-717-230 Sequence 230, App
38 68 34.3 2450 4 US-09-201-936-39 Sequence 39, Appli
39 68 34.3 2474 4 US-09-011-356-39 Sequence 39, Appli
40 68 34.3 2474 4 US-09-672-717-226 Sequence 226, App
41 68 34.3 2676 3 US-09-212-971-11 Sequence 11, Appli
42 68 34.3 2676 3 US-08-800-929A-11 Sequence 11, Appli
43 68 34.3 2676 4 US-09-617-053A-11 Sequence 1, Appli
44 65.8 33.2 1435 5 PCT-US95-05922A-1 Sequence 7, Appli
45 65.8 33.2 2580 2 US-08-511-485-7

ALIGNMENTS

RESULT 1

US-08-511-485-9
; Sequence 9, Application US/08511485
; Patent No. 5919312
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-511-485-9

Query Match 100.0%; Score 198; DB 2; Length 2100;
Best Local Similarity 100.0%; Pred. No. 1.6e-61;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGGTACTTTTGGAACTGATATCTACTGTTTACAGGAGCGCTT 60

Db 916 TATGAGCAGCGATCGTTACTTTTGGACATGGATATACCTCAGTTAAACAGGAGCAGCTT 975
QY 61 GCAAGAGCTGATTTATGCTTTTAGGTGAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 120
Db 976 GCAAGAGCTGATTTATGCTTTTAGGTGAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 1035
QY 121 GGAGGGCTCAGCGATTGGAAGCCCAAGTGAAGACCCCTGGGACACGAGATGTAAGTGTCTAC 180
Db 1036 GGAGGGCTCAGCGATTGGAAGCCCAAGTGAAGACCCCTGGGACACGAGATGTAAGTGTCTAC 1095
QY 181 CCAGGGTGCAAAATACCTA 198
Db 1096 CCAGGGTGCAAAATACCTA 1113

RESULT 2

US-09-201-936-9
; Sequence 9, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201.936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011.356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576.956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511.485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-9

Query Match 100.0%; Score 198; DB 4; Length 2100;
Best Local Similarity 100.0%; Pred. No. 1.6e-61;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAGCAGCGATCGTTACTTTTGGACATGGATATACCTCAGTTAAACAGGAGCAGCTT 60
Db 916 TATGAGCAGCGATCGTTACTTTTGGACATGGATATACCTCAGTTAAACAGGAGCAGCTT 975
QY 61 GCAAGAGCTGATTTATGCTTTTAGGTGAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 120
Db 976 GCAAGAGCTGATTTATGCTTTTAGGTGAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 1035
QY 121 GGAGGGCTCAGCGATTGGAAGCCCAAGTGAAGACCCCTGGGACACGAGATGTAAGTGTCTAC 180
Db 1036 GGAGGGCTCAGCGATTGGAAGCCCAAGTGAAGACCCCTGGGACACGAGATGTAAGTGTCTAC 1095
QY 181 CCAGGGTGCAAAATACCTA 198
Db 1096 CCAGGGTGCAAAATACCTA 1113

RESULT 3

US-09-011-356-9
; Sequence 9, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.

; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011.356A
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576.956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511.485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-011-356-9

Query Match 100.0%; Score 198; DB 4; Length 2100;
Best Local Similarity 100.0%; Pred. No. 1.6e-61;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAGCAGCGATCGTTACTTTTGGACATGGATATACCTCAGTTAAACAGGAGCAGCTT 60
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Db 976 GCAAGAGCTGATTTATGCTTTTAGGTGAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 1035
QY 121 GGAGGGCTCAGCGATTGGAAGCCCAAGTGAAGACCCCTGGGACACGAGATGTAAGTGTCTAC 180
Db 1036 GGAGGGCTCAGCGATTGGAAGCCCAAGTGAAGACCCCTGGGACACGAGATGTAAGTGTCTAC 1095
QY 181 CCAGGGTGCAAAATACCTA 198
Db 1096 CCAGGGTGCAAAATACCTA 1113

RESULT 4

US-09-672-717-224
; Sequence 224, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Lacasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; FILE OF INVENTION: Thereof
; FILE REFERENCE: 07891/025001
; CURRENT APPLICATION NUMBER: US/09/672.717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 224
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-672-717-224

Query Match 100.0%; Score 198; DB 4; Length 2100;
Best Local Similarity 100.0%; Pred. No. 1.6e-61;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAGCAGCGATCGTTACTTTTGGACATGGATATACCTCAGTTAAACAGGAGCAGCTT 60
Db 916 TATGAGCAGCGATCGTTACTTTTGGACATGGATATACCTCAGTTAAACAGGAGCAGCTT 975

APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Teang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 2691
TYPE: DNA
ORGANISM: Mus musculus
US-09-617-053A-9

Query Match 98.4%; Score 194.8; DB 4; Length 2691;
Best Local Similarity 99.0%; Pred. No. 2.6e-60;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGATCGTTACTTTTGGACATGATATACCTCAGTTAAACAGGAGCAGCTT 60
DB 1461 TATGAGCAGCGATCGTTACTTTTGGACATGATATACCTCAGTTAAACAGGAGCAGCTT 1520

QY 61 GCAAGAGCTGGATTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGA 120
DB 1521 GCAAGAGCTGGATTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGA 1580

QY 121 GGAGGCTCAGGATTCGAGCCAGGAGAGCCCTGGACAGCATGCTTAAGTGCTAC 180
DB 1581 GGAGGCTCAGGATTCGAGCCAGGAGAGCCCTGGACAGCATGCTTAAGTGCTAC 1640

QY 181 CCAGGTCGAATACCTA 198
DB 1641 CCAGGTCGAATACCTA 1658

RESULT 8
US-09-239-867-3
Sequence 3, Application US/09239867
Patent No. 6331412
GENERAL INFORMATION:
APPLICANT: Robert G. Korneluk et al.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
TITLE OF INVENTION: MALE FERTILITY
FILE REFERENCE: 07891/018002
CURRENT APPLICATION NUMBER: US/09/239,867
CURRENT FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/073,001
PRIOR FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1588
TYPE: DNA
ORGANISM: Homo sapiens
US-09-239-867-3

Query Match 87.4%; Score 173; DB 4; Length 1588;
Best Local Similarity 92.4%; Pred. No. 1.5e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGATCGTTACTTTTGGACATGATATACCTCAGTTAAACAGGAGCAGCTT 60
DB 826 TATGAGCAGCGATCGTTACTTTTGGACATGATATACCTCAGTTAAACAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGA 120
DB 886 GCAAGAGCTGGATTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGA 945

QY 121 GGAGGCTCAGCGATTCGAGCCAGGAGAGCCCTGGACAGCATGCTTAAGTGCTAC 180
DB 946 GGAGGCTCAGCGATTCGAGCCAGGAGAGCCCTGGACAGCATGCTTAAGTGCTAT 1005

QY 181 CCAGGTCGAATACCT 197
DB 1006 CCAGGTCGAATATCT 1022

RESULT 9
US-09-016-434-1053
Sequence 1053, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1053:
SEQUENCE CHARACTERISTICS:
LENGTH: 1659 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENE BANK
CLONE: GI016687
US-09-016-434-1053

Query Match 87.4%; Score 173; DB 4; Length 1659;
Best Local Similarity 92.4%; Pred. No. 1.5e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGATCGTTACTTTTGGACATGATATACCTCAGTTAAACAGGAGCAGCTT 60
DB 874 TATGAGCAGCGATCGTTACTTTTGGACATGATATACCTCAGTTAAACAGGAGCAGCTT 933

QY 61 GCAAGAGCTGGATTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGA 120
DB 934 GCAAGAGCTGGATTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGA 993

QY 121 GGAGGCTCAGCGATTCGAGCCAGGAGAGCCCTGGACAGCATGCTTAAGTGCTAC 180
DB 994 GGAGGCTCAGCGATTCGAGCCAGGAGAGCCCTGGACAGCATGCTTAAGTGCTAT 1053

US-09-201-936-3

Query Match 87.4%; Score 173; DB 4; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.9e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCGTTACTTTTGGACATGGATATACCTCAGTTAAACAGGAGCAGCTT 60
DB TATGAAGCAGGATCGTTACTTTTGGACATGGATATACCTCAGTTAAACAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 120
DB GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 945
QY 121 GGAGGGCTCAGGATTTGAAGCGCATAAAGTGAAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 180
DB GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 945
QY 121 GGAGGGCTCAGGATTTGAAGCGCATAAAGTGAAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 180
DB GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 945
QY 181 CCAGGGTGCAAAATACCT 197
DB CCAGGGTGCAAAATATCT 1022

RESULT 13

US-09-023-655-900
; Sequence 900, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Selihamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 5.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; PILLING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 900:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2540 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1184319
US-09-023-655-900

Query Match 87.4%; Score 173; DB 4; Length 2540;

Best Local Similarity 92.4%; Pred. No. 1.9e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCGTTACTTTTGGACATGGATATACCTCAGTTAAACAGGAGCAGCTT 60
DB TATGAAGCAGGATCGTTACTTTTGGACATGGATATACCTCAGTTAAACAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 120
DB GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 945
QY 121 GGAGGGCTCAGGATTTGAAGCGCATAAAGTGAAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 180
DB GGAGGGCTCAGGATTTGAAGCGCATAAAGTGAAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 1005
QY 181 CCAGGGTGCAAAATACCT 197
DB CCAGGGTGCAAAATATCT 1022

RESULT 14

US-09-011-356-3
; Sequence 3, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)...(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-011-356-3

Query Match 87.4%; Score 173; DB 4; Length 2540;

Best Local Similarity 92.4%; Pred. No. 1.9e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCGTTACTTTTGGACATGGATATACCTCAGTTAAACAGGAGCAGCTT 60
DB TATGAAGCAGGATCGTTACTTTTGGACATGGATATACCTCAGTTAAACAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 120
DB GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 945
QY 121 GGAGGGCTCAGGATTTGAAGCGCATAAAGTGAAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 180
DB GGAGGGCTCAGGATTTGAAGCGCATAAAGTGAAGCGCATAAAGTGAAGTGCCTTCCACTGTGGA 1005
QY 181 CCAGGGTGCAAAATACCT 197
DB CCAGGGTGCAAAATATCT 1022

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RESULT 15
US-09-672-717-218
; Sequence 218, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; FILE OF INVENTION: Thereof
; FILE REFERENCE: 07891/025001
; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 218
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2540)
; OTHER INFORMATION: n=a,t,c, or g
US-09-672-717-218

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Query Match      87.4%; Score 173; DB 4; Length 2540;
Best Local Similarity 92.4%; Pred No. 1.9e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATACTCAGTTAAAGGAGCAGCTT 60
Db 826 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATACTCAGTTAAAGGAGCAGCTT 885

Qy 51 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCCACTGTGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCCACTGTGA 945

Qy 121 GGAGGGCTCAGGATTGGAGCCAGTGAAGACCCCTGGGACGAGCATGCTAAGTGCTAC 180
Db 946 GGAGGGCTCAGGATTGGAGCCAGTGAAGACCCCTGGGACGAGCATGCTAAGTGCTAC 1005

Qy 181 CCAGGGTGCAATACCT 197
Db 1006 CCAGGGTGCAATATCT 1022

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Search completed: March 13, 2004, 06:26:52
Job time : 63 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 13, 2004, 04:27:28 ; Search time 207 Seconds
(without alignments)
3521.528 Million cell updates/sec

Title: US-09-654-743-51

Perfect score: 198
Sequence: 1 tatgaacacgagtcgttac.....accacgggtgcaataaccta 198

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2432557 seqs, 1840798884 residues

Total number of hits satisfying chosen parameters: 4865114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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- 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	100.0	2100	9	US-09-201-936-9
2	194.8	98.4	2691	9	US-09-974-592-9
3	173	87.4	1659	15	US-10-305-720-1053
4	173	87.4	2404	9	US-09-964-899-38
5	173	87.4	2540	9	US-09-201-936-3
6	173	87.4	2540	14	US-10-007-926A-274
7	173	87.4	5232	9	US-09-974-592-3
c 8	134.4	67.9	152331	13	US-10-095-407-16
9	109.6	55.4	176373	13	US-10-095-407-17
c 10	76	38.4	255	14	US-10-102-524-906
11	76	38.4	2563	15	US-10-305-720-1076
12	76	38.4	2601	14	US-10-232-286-3
13	76	38.4	2676	9	US-09-201-936-5
14	76	38.4	2916	12	US-10-240-425-1436
15	76	38.4	3076	9	US-09-954-456-1635

16	76	38.4	3076	9	US-09-954-531-16	Sequence 16, Appl
17	76	38.4	3076	14	US-10-197-280-1	Sequence 1, Appl
18	76	38.4	3076	15	US-10-388-263-157	Sequence 157, App
19	76	38.4	3164	14	US-10-141-618-5	Sequence 5, Appl
20	76	38.4	3165	14	US-10-269-909-5	Sequence 5, Appl
21	76	38.4	3734	14	US-10-353-461-7	Sequence 7, Appl
22	76	38.4	5844	10	US-09-971-392-253	Sequence 253, App
23	76	38.4	5857	14	US-10-247-671-18	Sequence 18, Appl
24	76	38.4	6669	9	US-09-974-592-5	Sequence 5, Appl
25	68	34.3	2450	9	US-09-201-936-39	Sequence 39, Appl
26	68	34.3	2676	9	US-09-974-592-11	Sequence 11, Appl
27	66	33.3	7990	14	US-10-311-455-131	Sequence 131, App
28	66	33.3	7990	14	US-10-240-452-7	Sequence 7, Appl
29	65.8	33.2	1435	8	US-08-464-588-1	Sequence 1, Appl
30	65.8	33.2	1435	14	US-10-323-643-1	Sequence 1, Appl
31	65.8	33.2	2531	14	US-10-207-635-199	Sequence 199, App
32	65.8	33.2	2580	9	US-09-201-936-7	Sequence 7, Appl
33	65.8	33.2	2589	14	US-10-232-286-1	Sequence 1, Appl
34	65.8	33.2	3496	14	US-10-153-668-337	Sequence 337, App
35	65.8	33.2	3532	9	US-09-880-107-3354	Sequence 3354, Ap
36	65.8	33.2	3532	15	US-10-464-158-1	Sequence 1, Appl
37	65.8	33.2	3732	9	US-09-974-592-7	Sequence 7, Appl
38	65.8	33.2	4614	10	US-09-814-383-19934	Sequence 19934, A
39	61	30.8	2862	14	US-10-232-286-13	Sequence 13, Appl
40	61	30.8	3151	9	US-09-974-592-13	Sequence 13, Appl
41	59.4	30.0	2416	9	US-09-201-936-41	Sequence 41, Appl
42	56.4	28.5	3773	14	US-10-041-859-1	Sequence 1, Appl
c 43	54.8	27.7	7990	14	US-10-311-455-132	Sequence 132, App
c 44	54.8	27.7	7990	14	US-10-240-452-8	Sequence 8, Appl
45	53.2	26.9	843	14	US-10-244-586-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-201-936-9
; Sequence 9, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Lisbon, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-9

Query Match 100.0%; Score 198; DB 9; Length 2100;
Best Local Similarity 100.0%; Pred. No. 9.5e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAACACGAGTCGTTACTTTTGGACATGATATCTCAGTTAACAGGACGAGCTT 60
DB 916 TATGAACACGAGTCGTTACTTTTGGACATGATATCTCAGTTAACAGGACGAGCTT 975

Query Match 87.4%; Score 173; DB 9; Length 5232;
Best Local Similarity 92.4%; Pred. No. 8.5e-50;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCGTTACTTTTGGACATGATATACCTAGTTAAACAGGAGCAGCTT 60
DB 826 TATGAAGCAGGATCGTTACTTTTGGACATGATATACCTAGTTAAACAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGCGATTAAGTGAAGTCTTCCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGCGATTAAGTGAAGTCTTCCACTGTGGA 945

QY 121 GGAGGCTCAGGATGGAAGCCAGTGAAGACCCCTGGACACGATGCTAAGTGTCTAC 180
DB 946 GGAGGCTCAGTATGGAAGCCAGTGAAGACCCCTGGACACGATGCTAAGTGTCTAT 1005

QY 181 CCAGGGTGCAATACCT 197
DB 1006 CCAGGGTGCAATATCT 1022

RESULT 8
US-10-095-407-16/c
; Sequence 16, Application US/10095407
; Publication No. US20020164330A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/10/095,407
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/091,650
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/054,646
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 152331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
US-10-095-407-16

Query Match 67.9%; Score 134.4; DB 13; Length 152331;
Best Local Similarity 83.2%; Pred. No. 1.4e-35;
Matches 164; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

QY 1 TATGAAGCAGGATCGTTACTTTTGGACATGATATACCTAGTTAAACAGGAGCAGCTT 60
DB 3298 TATGAAGCAGGATCGTTACTTTTGGGATGTGGATATATTCAGTTAAACAGGAGCAGCTT 3239

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGCGATTAAGTGAAGTCTTCCACTGTGGA 120
DB 3238 TCAAGAGCTGGATTTATGCTTTAGGTGAAGGCGATTAAGTGAAGTCTTCCACTGTGGA 3179

QY 121 GGAGGCTCAGGATGGAAGCCAGTGAAGACCCCTGGACACGATGCTAAGTGTCTAC 180
DB 3178 GGGGGCTTACTGATTTGGACCCACCAGAA-ACCTTTGGGACACATATAATATGGAT 3120

QY 181 CCAGGGTGCAATACCT 197
DB 3119 CCANGGTGTAAATATCT 3103

RESULT 9
US-10-095-407-17
; Sequence 17, Application US/10095407
; Publication No. US20020164330A1

GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/10/095,407
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/091,650
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/054,646
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
US-10-095-407-17

Query Match 55.4%; Score 109.6; DB 13; Length 176373;
Best Local Similarity 86.4%; Pred. No. 7.5e-27;
Matches 121; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 58 CTTTGAAGAGCTGGATTTATGCTTTAGGTGAAGGCGATTAAGTGAAGTCTTCCACTGT 117
DB 12549 CTTTGAAGAGCTGGATTTATGCTTTAGGTGAAGGCGATTAAGTGAAGTCTTCCACTGT 12608

QY 118 GGAGGAGGCTCAGGATGGAAGCCAGTGAAGACCCCTGGACACGATGCTAAGTGC 177
DB 12609 GGAGGAGGCTCAGTGAAGCCAGTGAAGACCCCTGGACACGATGCTAAGTGC 12668

QY 178 TACCCAGGCTGCAATACCT 197
DB 12669 CATCCAGGCTGCAATATCT 12688

RESULT 10
US-10-102-524-906/c
; Sequence 906, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Gaiger, Alexander
; APPLICANT: Gordon, Brian
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF KIDNEY CANCER
; FILE REFERENCE: 210121.572
; CURRENT APPLICATION NUMBER: US/10/102,524
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 1863
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 906
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-102-524-906

Query Match 38.4%; Score 76; DB 14; Length 255;
Best Local Similarity 67.9%; Pred. No. 2.5e-16;
Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 42 AGTTAAACAGGAGCAGCTTCCAGAGCTGGATTTATGCTTTAGGTGAAGGCGATTAAGT 101
DB 223 AGTTAACTCTGAGCAGCTTCCAAAGTCGGGCTTTTATATGTTGGTAAACAGTATGATGT 164

QY 102 GAAGTGTCTCCACTGTGGAGAGGCTCAGCGATTGGAGCCCAAGTGAAGACCCCTGGGA 161

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Db 163 CAATGCTTTTCTGTGATGGTGACCTCAGGTGTGGGATCTGGAGATGATCCATGGCT 104
QY 162 CCAGATGCTAAAGTGTACCCAGGGTCCAAATACCT 197
Db 103 TCAACATGCCAAGTGGTTTCCAGGTTGTGATGACTT 68

RESULT 11
US-10-305-720-1076
; Sequence 1076, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; FILE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; CURRENT APPLICATION NUMBER: US/10/305,720
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1076
; LENGTH: 2563
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g1160974
US-10-305-720-1076

Query Match 38.4%; Score 76; DB 15; Length 2563;
Best Local Similarity 67.9%; Pred. No. 6.9e-16;
Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 42 AGTTAAACAAGGACGAGCTTGCAGAGCTGGATTTTATGCTTTTAGGTGAAGGCGATAAAGT 101
Db 932 AGTTAATCCTGACGAGCTTGCAGTGGGGTTTTATTATGTGGTTAACAGTATGATCT 991
QY 102 GAAGTGTCTCACTGTGAGAGGGCTCAGGATTTGAACCAAGTGAAGACCCCTGGGA 161
Db 992 CAAATGCTTTTGTGTGATGGTGACTCAGGTGTGGGAATCTGGAGATGATCCATGGCT 1051
QY 162 CCAGATGCTAAAGTGTACCCAGGGTCCAAATACCT 197
Db 1052 TCAACATGCCAAGTGGTTTCCAGGTTGTGATGACTT 1087

RESULT 12
US-10-232-286-3
; Sequence 3, Application US/10232286
; Publication No. US20030143579A1
; GENERAL INFORMATION:
; APPLICANT: Roths, Mike
; TITLE OF INVENTION: David V Goeddel, Inhibitors of Apoptosis
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/232,286
; FILING DATE: 30-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/08/569,749
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-232-286-3

Query Match 38.4%; Score 76; DB 14; Length 2601;
Best Local Similarity 67.9%; Pred. No. 7e-16;
Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 42 AGTTAAACAAGGACGAGCTTGCAGAGCTGGATTTTATGCTTTTAGGTGAAGGCGATAAAGT 101
Db 932 AGTTAATCCTGACGAGCTTGCAGTGGGGTTTTATTATGTGGTTAACAGTATGATCT 991
QY 102 GAAGTGTCTCACTGTGAGAGGGCTCAGGATTTGAACCAAGTGAAGACCCCTGGGA 161
Db 992 CAAATGCTTTTGTGTGATGGTGACTCAGGTGTGGGAATCTGGAGATGATCCATGGCT 1051
QY 162 CCAGATGCTAAAGTGTACCCAGGGTCCAAATACCT 197
Db 1052 TCAACATGCCAAGTGGTTTCCAGGTTGTGATGACTT 1087

RESULT 13
US-09-201-936-5
; Sequence 5, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/1B96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2676
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: variation
; LOCATION: (2470)...(2470)
; OTHER INFORMATION: N may be any nucleotide
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2476)...(2476)
; OTHER INFORMATION: N may be any nucleotide
; FEATURE:
```


NAME/KEY: variation
LOCATION: (2483)...(2483)
OTHER INFORMATION: N may be any nucleotide
FEATURE:
NAME/KEY: variation
LOCATION: (2602)...(2602)
OTHER INFORMATION: N may be any nucleotide
US-09-201-936-5

Query Match 38.4%; Score 76; DB 9; Length 2676;
Best Local Similarity 67.9%; Pred. No. 7.1e-16;
Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 42 AGTTAAACAGAGCAGCTTCAGAGAGCTGATTTTATGCTTTAGGTGAAGCGATAAAGT 101
DB 998 AGTTAACTGAGCAGCTTCAGAGTGGGGTTTTTATGCTGGGTAAACAGTATGATGT 1057
QY 102 GAAGTCTTCCACTGTGGAGAGGGCTTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGGA 161
DB 1058 CAATGCTTTTCTGTGATGTGAGCTCAGGTGTGGGAATCTGGAGATGATCCATGGGT 1117
QY 162 CCAGATGCTAAGTGCTACCCAGGGTCAATACCT 197
DB 1118 TCAACATGCCAAGTGGTTTCCAGGTGTGATGACTT 1153

RESULT 14
US-10-240-425-1436
Sequence 1436, Application US/10240425
Publication No. US20040033502A1

GENERAL INFORMATION:
APPLICANT: Williams, Amanda
APPLICANT: Bolland, Joseph F.
APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
APPLICANT: Wetzel, Jon C.
APPLICANT: Scherif, Uwe
APPLICANT: Vockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
FILE REFERENCE: 44921-5026
CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/193,446
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1436
LENGTH: 2916
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20040033502A1 U45878
FEATURE:
NAME/KEY: unsure
LOCATION: (1)...(2907)
OTHER INFORMATION: n = a or c or g or t
US-10-240-425-1436

Query Match 38.4%; Score 76; DB 12; Length 2916;
Best Local Similarity 67.9%; Pred. No. 7.3e-16;
Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 42 AGTTAAACAGAGCAGCTTCAGAGAGCTGATTTTATGCTTTAGGTGAAGCGATAAAGT 101
DB 1258 AGTTAACTGAGCAGCTTCAGAGTGGGGTTTTTATGCTGGGTAAACAGTATGATGT 1317
QY 102 GAAGTCTTCCACTGTGGAGAGGGCTTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGGA 161
DB 1318 CAATGCTTTTCTGTGATGTGAGCTCAGGTGTGGGAATCTGGAGATGATCCATGGGT 1377
QY 162 CCAGATGCTAAGTGCTACCCAGGGTCAATACCT 197

DB 1378 TCACATGCCAAGTGGTTTCCAAAGGTGTGATGACTT 1413

RESULT 15

US-09-954-456-1635
Sequence 1635, Application US/09954456
Patent No. US20020115057A1

GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: Patent In version 3.0
SEQ ID NO 1635
LENGTH: 3076
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-1635

Query Match 38.4%; Score 76; DB 9; Length 3076;
Best Local Similarity 67.9%; Pred. No. 7.5e-16;
Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 42 AGTTAAACAGAGCAGCTTCAGAGAGCTGATTTTATGCTTTAGGTGAAGCGATAAAGT 101
DB 1534 AGTTAACTGAGCAGCTTCAGAGTGGGGTTTTTATGCTGGGTAAACAGTATGATGT 1593
QY 102 GAAGTCTTCCACTGTGGAGAGGGCTTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGGA 161
DB 1594 CAATGCTTTTCTGTGATGTGAGCTCAGGTGTGGGAATCTGGAGATGATCCATGGGT 1653
QY 162 CCAGATGCTAAGTGCTACCCAGGGTCAATACCT 197
DB 1654 TCAACATGCCAAGTGGTTTCCAAAGGTGTGATGACTT 1689

Search completed: March 13, 2004, 06:34:01
Job time : 208 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 13, 2004, 04:02:03 ; Search time 2177.5 Seconds

(without alignments)
2715.367 Million cell updates/sec

Title: US-09-654-743-51

Perfect score: 198

Sequence: 1 tatgaagcaggtatcttac.....accagggtgcaataaccta 198

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthm:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estc:*

9: gb_estl:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pla:*

20: em_gss_rtt:*

21: em_gss_fun:*

22: em_gss_man:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vri:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	176.8	89.3	773	14	CD350778 UI-M-GIO-
2	168	84.8	628	9	AI573382 mn83e12.x
3	149	75.3	1805	11	BC039318 Homo sapi
4	149	75.3	1851	11	BC056914 Homo sapi

5	147.4	74.4	1789	11	BC046168
6	108	54.5	617	10	BB663325
7	103.4	52.2	504	10	BB650856
8	100.8	50.9	318	10	BF659610
c	98	49.5	334	12	BM220130
c	98	49.5	584	13	BO552032
11	92.2	46.6	1177	12	BM805359
12	90.2	45.6	536	9	AUI23207
13	88.2	44.5	791	14	CF222542
14	87	43.9	373	13	BY662508
15	85.2	43.0	849	28	BZ242580
16	84.2	42.5	716	9	AV706807
17	81.8	41.3	1472	29	AX398945
18	80.4	40.6	1494	29	AX398943
c	76.2	38.5	721	29	CH100865
20	76.2	38.5	663	13	BU658508
21	76	38.4	341	10	AW375598
22	76	38.4	354	10	AW375594
23	76	38.4	402	10	AW846507
24	76	38.4	531	10	AW375599
25	76	38.4	532	10	AW846425
26	76	38.4	546	10	AW846421
27	76	38.4	571	10	AW375649
c	76	38.4	582	10	AW846337
29	76	38.4	590	10	BZ268377
30	76	38.4	621	10	AW375648
31	76	38.4	680	10	AW375625
32	76	38.4	886	13	BO652590
33	76	38.4	1799	29	AY420753
34	75.2	38.0	269	10	BES08790
35	72.4	36.6	690	29	CB697566
36	71.2	36.0	275	29	CG545804
37	70.4	35.6	1748	29	AY420754
38	69.2	34.9	567	12	BI961039
39	69	34.8	735	14	CD284353
c	68.4	34.5	420	28	AQ011995
41	68	34.3	323	10	BES47058
42	68	34.3	385	10	BE851680
43	68	34.3	450	14	CA559631
44	68	34.3	557	9	AA197349
45	68	34.3	586	14	CF913919

ALIGNMENTS

RESULT 1
CD350778
LOCUS
DEFINITION
CD350778.1 GI:31142365
ACCSSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CD350778 773 bp mRNA linear EST 09-JUL-2003
UI-M-GIO-cgh-g-23-0-UI.r1 NIH.BMAP_GIO Mus musculus cDNA clone
IMAGE:6853392 5', mRNA sequence.

CD350778
CD350778.1 GI:31142365
EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Muridae; Mus.

1 (bases 1 to 773)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@bcr@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pYX-5.

FEATURES
source

Location/Qualifiers

1. .773
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="C57BL/6"
/clone="IMAGE:6853392"
/tissue_type="whole brain"
/lab_host="embryo 13.5, 14.5, 16.5, 17.5dpc"
/clone_lib="NIH BMAP G10"
/notes="Organ: Brain; Vector: pYX-Asc; Site: 1: Ecov 1; Site 2: Not 1; The library was constructed according to Bonaldo, Lemmon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecov I adaptor, digested with Not I and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 89.3%; Score 176.8; DB 14; Length 773;
Best Local Similarity 96.3%; Pred. No. 8.1e-45;
Matches 181; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 11 CGATCGTTACTTTGGACATGGATATACCTCAGTTAAACAGGAGCAGCTTGCAGAGCTG 70
DB 1 GATCGTTACTTTGGACATGGACATCCCTCAGTTAAACAGGAGCAGCTTGCAGAGCTG 60

QY 71 GATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTCTTCCATGTFGGAGGAGGCTCA 130
DB 61 GATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTCTTCCATGTFGGAGGAGGCTCA 120

QY 131 CGATTTGAAGCCAGTGAAGACCCCTGGACACGAGCTGTAAGTCTCCAGGCTGCA 190
DB 121 CGATTTGAAGCCAGTGAAGACCCCTGGGAAACAGCATGCGAAGTGTGATCCAGGCTGCA 180

QY 191 AATACCTA 198
DB 181 AATACCTA 188

RESULT 2

AI573382/c
LOCUS
DEFINITION
mn83e12.x1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone
IMAGE:550702 3' similar to TR:Q60989 Q60989 MIHA. ; mRNA sequence.

ACCESSION
AI573382
VERSION
AI573382.1 GI:4536756
SOURCE
EST.
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 628)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, N., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999

TITLE

JOURNAL

COMMENT

Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

FEATURES
source

1. .628
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:550702"
/tissue_type="Tcell"
/dev_stage="W30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse Tcell 937311"
/notes="Organ: Blood; Vector: pBluescript SK-; Site 1: Ecov I; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"

ORIGIN

Query Match 84.8%; Score 168; DB 9; Length 628;
Best Local Similarity 93.4%; Pred. No. 4.4e-42;
Matches 185; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 1 TATGAAGCAGGATCGTTACTTTTGAACATGGATATACCTCAGTTAAACAGGAGCAGCTT 60
DB 604 TATGAAGCAGGATCGTTACTTTTGAACATGGATATACCTCAGTTAAACAGGAGCAGCTT 545

QY 61 GCAAGAGCTCGATTTTATGCTTTAGTGAAGGCGATAAAGTGAAGTCTTCCATGTTGGA 120
DB 544 GCAAGAGCT-GATTTTATGCTTTAGTGAAGGCGATAAAGTGAAGTCTTCCATGTTGGA 486

QY 121 GGAGGGCTCAGGATTTGGAAGCCCAAGTGAAGACCCCTGGACACGATCTTAAGTGCTAC 180
DB 485 GGAGGGCTCAGGATTTGGAAGCCCAAGTGAAGACCCCTGGGAAACAGCATCGGAAGTGGTAC 426

QY 181 CCAGGGTGCAAAATACCTA 198
DB 425 NCAGGGTGCAAAATACCTA 408

RESULT 3

BC039318
LOCUS
DEFINITION
Homo sapiens, Similar to baculoviral IAP repeat-containing 8, clone
IMAGE:5269405, mRNA.

ACCESSION
BC039318
VERSION
BC039318.1 GI:25058167
SOURCE
HTC.
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1805)
Strausberg, R.
Direct Submission

TITLE

JOURNAL

COMMENT

REMARK

COMMENT

Submitted (01-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>

Fax: 314 286 1810

Email: museest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Possible reversed clone: similarity on wrong strand

High quality sequence stop: 440.

Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 74 Row: h Column: 10
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein
This clone has the following problem: frame shifted.

FEATURES

source
1..1805
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5269405"
/tissue_type="Testis"
/clone_lib="NIH MGC_97"
/lab_host="DH10B"
/note="Vector: pBluescript"

ORIGIN

Query Match 75.3%; Score 149; DB 11; Length 1805;
Best Local Similarity 84.8%; Pred. No. 7.6e-36;
Matches 167; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGAAACATGATATACCTTACCAAGGAGCAGCTT 60
Db 1028 TATGAAGCAGCGATCGTTACTTTTGGAAACATGATATACCTTACCAAGGAGCAGCTT 1087

QY 61 GCAAGAGCTGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
Db 1088 GCAAGAGCTGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 1147

QY 121 GGAGGCTCAGCGATTGGAAGCCCAAGTGAAGCCCTGGACGAGCATGCTAAGTCTAC 180
Db 1148 GGAGGCTCAGCGATTGGAAGCCCAAGTGAAGCCCTGGACGAGCATGCTAAGTCTAC 1207

QY 181 CCAGGCTGCAATACCT 197
Db 1208 CCAGGCTGCAATATCT 1224

RESULT 4
BC056914
LOCUS
DEFINITION 1851 bp mRNA linear HTC 16-SEP-2003
BC056914
Hom sapiens baculoviral IAP repeat-containing 8, mRNA (CDNA clone
IMAGE:5742924).

ACCESSION BC056914
VERSION BC056914.1 GI:3478469
KEYWORDS HTC.
SOURCE Hom sapiens (human)
ORGANISM Hom sapiens

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1851)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.D., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

TITLE

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
JOURNAL
TITLE

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Nees, Pawan Pandoh, Anna-Liisa Prabhhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 119 Row: h Column: 2
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 16974127
This clone has the following problem: retained intron.

FEATURES

source

1..1851
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5742924"
/tissue_type="Brain, adult medulla"
/clone_lib="NIH MGC_119"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 75.3%; Score 149; DB 11; Length 1851;
Best Local Similarity 84.8%; Pred. No. 7.7e-36;
Matches 167; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGAAACATGATATACCTTACCAAGGAGCAGCTT 60
Db 1062 TATGAAGCAGCGATCGTTACTTTTGGAAACATGATATACCTTACCAAGGAGCAGCTT 1121

QY 61 GCAAGAGCTGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
Db 1122 GCAAGAGCTGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 1181

QY 121 GGAGGCTCAGCGATTGGAAGCCCAAGTGAAGCCCTGGACGAGCATGCTAAGTCTAC 180
Db 1182 GGAGGCTCAGCGATTGGAAGCCCAAGTGAAGCCCTGGACGAGCATGCTAAGTCTAC 1241

QY 181 CCAGGCTGCAATACCT 197
Db 1242 CCAGGCTGCAATATCT 1258

RESULT 5
BC046168

LOCUS BC046168 1789 bp mRNA linear HTC 13-FEB-2003
 DEFINITION Homo sapiens, similar to baculoviral IAP repeat-containing 8, clone IMAGE:5742590, mRNA.

ACCESSION BC046168
 VERSION BC046168.1 GI:28374455
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1789)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (31-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www.shgc.stanford.edu>
 Contact: (Dickson, Mark) mcdeapaxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 107 Row: i Column: 1
 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein
 This clone has the following problem: frame shifted.

FEATURES
 source
 1..1789
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5742590"
 /tissue_type="Brain, adult medulla"
 /clone_lib="NIH MGC 119"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

ORIGIN
 Query Match 74.4%; Score 147.4; DB 11; Length 1789;
 Best Local Similarity 84.3%; Fred. No. 2.4e-35;
 Matches 166; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGATATACTCAGTTAAACAAGGACGAGCTT 60
 DB |||||
 1002 TATGAAGCCGCGCTCATTTACTTTTGGGACATGGATGACTCCGTCACAAAGAGCAGCTT 1061
 QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTCAAGCCGATTAAGTGAAGTCTTCCACTGTGGA 120
 DB |||||
 1062 GCAAGAGCTGGATTTTATGCTTATAGGTCAAGGAGGATAAGTACAGTCTTCTACTGTGGA 1121
 QY 121 GGAGGGCTCACGGATTGGAAGCAAGTGAAGACCCCTGGGACCAAGCATGCTAAAGTGTCTAC 180
 DB |||||
 1122 GGAGGGCTAGCAACTGGAGCCCAAGGAAGATCTTTGGGACAGCATGCTTAATGGTAT 1181
 QY 181 CCAGGGTGCATAATACCT 197
 DB |||||
 1182 CCAGGTTCGAATATCT 1198

RESULT 6
 BB663325 617 bp mRNA linear EST 26-OCT-2001
 LOCUS BB663325

DEFINITION BB663325 RIKEN full-length enriched, 15 days embryo head Mus musculus CDNA clone D930039G22 5', mRNA sequence.

ACCESSION BB663325
 VERSION BB663325.1 GI:16497079
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 617)
 AUTHORS Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ono, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 Unpublished (2001)

TITLE RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/,
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
 e mouse tissues.
 Location/Qualifiers
 1..617
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="D930039G22"
 /sex="mixed"
 /tissue_type="head"
 /dev_stage="15 days embryo"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, 15 days embryo head"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5."

FEATURES
 source

Email: cgapb-re@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 image.lnl.gov/image/html/iresources.shtml

MGI:1436942

Possible reversed clone: polyt not found

Seq primer: -40UP from Gibco

High quality sequence stop: 226.

FEATURES

Location/Qualifiers
 1..318
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="Czech II"
 /db_xref="taxon:10090"
 /clone="IMAGE:3676174"
 /tissue_type="spontaneous tumor, metastatic to mammary."
 Stem cell origin.
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Lu29"
 /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dn.
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 50.9%; Score 100.8; DB 10; Length 318;
 Best Local Similarity 93.8%; Pred. No. 5.6e-21;
 Matches 105; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 53 ACACGCTTGCAGACCTGATTTATGCTTTAGCTGAAGCGATAAAGTGAAGTCTTC 112
 Db 317 ACACCTTGCAGAGATTGGATTTTAAAGCTTTAGCTGAAGCGATAAAGTCAAGTCTTC 258
 QY 113 ACTGTGGAGGAGGCTACGAGTGGAAAGCCAGTGAAGCCCTCGGACCA 164
 Db 257 ACTGTGGAGGAGGCTCTCGGATGGAGCCAGTGAAGCCCTTGGGAACA 206

RESULT 9

BM220130/c
 LOCUS
 DEFINITION
 BM220130 334 bp mRNA linear EST 07-JUN-2003
 C0935E08-3 NIA Mouse 12.5-dpc Male Genital Ridge/Mesonephros cDNA
 Library (Long) Mus musculus cDNA clone NIA:C0935E08 IMAGE:30037975
 3', mRNA sequence.
 ACCESSION
 VERSION
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 334)
 Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
 Construction of long-transcript enriched cDNA libraries from
 submicrogram amounts of total RNAs by a universal PCR amplification
 method
 Genome Res. 11 (9), 1553-1558 (2001)
 21429098
 11544199
 On Dec 14, 2001 this sequence version replaced gi:17780130.
 Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@lgsun.grc.nia.nih.gov
 Plate: C0935 row: E column: 08
 Seq primer: -21M13 Forward
 High quality sequence stop: 334

FEATURES

Location/Qualifiers
 1..334
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="niaEST:C0935E08-3"
 /db_xref="taxon:10090"
 /clone="NIA:C0935E08 IMAGE:30037975"
 /sex="Male"
 /tissue_type="Male genital ridge/mesonephros"
 /dev_stage="12.5-dpc"
 /lab_host="DH10B"
 /clone_lib="NIA Mouse 12.5-dpc Male Genital
 Ridge/Mesonephros cDNA Library (Long)"
 /note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:
 NotI; Mouse cDNA project by the Laboratory of Genetics,
 National Institute on Aging (NIA), Intramural Research
 Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
 a long-transcript enriched cDNA library (Ref. Genome Res.
 11: 1553-1558 (2001). [PMID: 11544199]). Double-stranded
 cDNAs were synthesized with an Oligo(dT) primer
 [Invitrogen];
 5'-pGACTGCTCTAGTCGAGCGCGCCCTTTTCTTTT-3' from
 1.8 ug of total RNA, treated with T4 DNA polymerase and
 purified by ethanol-precipitation. The cDNAs were ligated
 to lone-linker IL-Sal4, purified by phenol/chloroform, and
 separated from free linkers by Centricon 100. Then, the
 cDNAs were amplified by long-range high fidelity PCR using
 Ex Taq polymerase (Takara) with a primer Sal4-S. The
 products were purified by phenol/chloroform and Centricon
 100. The cDNAs were digested with SalI and NotI enzymes
 and cloned into SalI/NotI site of pSPORT1 plasmid vector.
 The DH10B E. coli host was transformed with the ligation
 mixture by the standard chemical method. The average
 insert size is about 2.4 kb. The library was constructed
 by Yulan Piao (NIA)."

ORIGIN

Query Match 49.5%; Score 98; DB 12; Length 334;
 Best Local Similarity 95.3%; Pred. No. 4.4e-20;
 Matches 101; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 82 TTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGAGGAGGCTCAGGATTGGAAG 141
 Db 260 TTAGTGAAGCGGATAAAGTGAAGTCTTCACTGTGGAGGAGGCTCAGGATTGGAAG 201
 QY 142 CCAAGTGAAGACCCCTCGGACCGACGATGCTTAAGTGTCTACCCGGT 187
 Db 200 CCAAGTGAAGACCCCTTGGGAACAGCATGCGAGTGGTACCACGGT 155

RESULT 10

BQ552032/c
 LOCUS
 DEFINITION
 BQ552032 584 bp mRNA linear EST 20-JUN-2002
 H4013A06-3 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
 H4013A06 3', mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 584)
 VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G.,
 Martin, P.R., Stagg, C.A., Basse, U., Aiba, K., Hamatani, T.,
 Kargul, G.J., Luo, A.G., Kelsa, J., Hide, W. and Ko, M.S.H.
 Assembly, verification, and initial annotation of NIA 7.4K mouse
 cDNA clone set
 Genome Res. 12 (12), 1999-2003 (2002)
 22354164
 12466305

COMMENT

Other_ESTs: H4013A06-5
 Contact: Yong Qian
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.grc.nia.nih.gov
 This clone set has been freely distributed to the community. Please
 visit http://igsun.grc.nia.nih.gov/cdna/NIA_7_4k.html for details.
 Plate: H4013 row: A column: 06
 Seq primer: -21M13 Forward
 High quality sequence stop: 584
 POLYA=Yes.

FEATURES

Location/Qualifiers

source

1..584
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57Bl/6"
 /db_xref="niaEST:H4013A06-3"
 /db_xref="taxon:10090"
 /clone="H4013A06"
 /sex="mixed"
 /dev_stages="mixed"
 /lab_host="DH10B"
 /clone_lib="NIA Mouse 7.4K cDNA Clone Set"
 /note="Vector: pSPORT1; Site 1: Sali; Site 2: NotI; This
 clone is among a rearranged set of 7,407 clones from more
 than 20 cDNA libraries."

ORIGIN

Query Match 49.5%; Score 99; DB 13; Length 584;
 Best Local Similarity 95.3%; Pred. No. 5.8e-20;
 Matches 101; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 82 TTAGTGAAGCGATAAGTGAAGTGTCCACTGTGGAGGAGGCTCACGGATTGGAAG 141
 Db 260 TTAGTGAAGCGATAAGTGAAGTGTCCACTGTGGAGGAGGCTCACGGATTGGAAG 201
 QY 142 CCAAGTGAAGACCCCTGGGACGACATGCTAAGTGTACCCAGGT 187
 Db 200 CCAAGTGAAGACCCCTGGGACGACATGCTAAGTGTACCCAGGT 155

RESULT 11

BM805359
 LOCUS
 DEFINITION 1177 bp mRNA linear EST 05-MAR-2002
 AGENCOURT 6499731 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5728685
 5', mRNA sequence.

ACCESSION BM805359

VERSION BM805359.1 GI:19122182

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1177)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: Invitrogen

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM12724 row: m column: 06

High quality sequence stop: 409.

Location/Qualifiers

source

1..1177

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"
 /clone="IMAGE:5728685"
 /tissue_type="hippocampus"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_124"

/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: EcoRV
 (destroyed); Site 2: NotI; RNA source male hippocampus,
 age 27. Library is oligo-dT primed and directionally
 cloned (Scorv site is destroyed upon cloning). Average
 insert size 1.4 kb, insert size range 0.9-4 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 012."

ORIGIN

Query Match 46.6%; Score 92.2; DB 12; Length 1177;
 Best Local Similarity 88.5%; Pred. No. 5.6e-18;
 Matches 100; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 85 GGTGAAGCGGATAAAGTGAAGTGTCCACTGTGGAGGAGGCTCACGGATTGGAAGCCA 144
 Db 142 GGTGAAGCGGATAAAGTGAAGTGTCCACTGTGGAGGAGGCTCACGGATTGGAAGCCA 201
 QY 145 AGTGAAGACCCCTGGGACGACATGCTAAGTGTACCCAGGTGCAATACCT 197
 Db 202 AGTGAAGACCCCTGGGACGACATGCTAAGTGTATCCAGGTGCAATATCT 254

RESULT 12

AUI23207
 LOCUS
 DEFINITION 536 bp mRNA linear EST 01-AUG-2002
 AUI23207 NT2RM1 Homo sapiens cDNA clone NT2RM1000921 5', mRNA
 sequence.

ACCESSION AUI23207

VERSION AUI23207.1 GI:10947923

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 536)

AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Kawai, Y., Ishii, S., Saito, K.,

Nakamura, Y., Nagai, T., Sugano, S., and Isogai, T.

HRI human cDNA project (Ota, T., Nishikawa, T., Suzuki, Y., Kawai, Y.,

Ishii, S., Saito, K., Nakamura, Y., Nagai, T., Sugano, S., Isogai, T.)

JOURNAL Unpublished (2000)

COMMENT Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.

Location/Qualifiers

source

1..536

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="NT2RM1000921"

/cell_type="teratocarcinoma"

/cell_line="NT2"

/clone_lib="NT2RM1"

/note="Vector: pUC19FL3; mRNA from uninduced NT2 neuronal

precursor cells"

ORIGIN

Query Match 45.6%; Score 90.2; DB 9; Length 536;
 Best Local Similarity 86.7%; Pred. No. 1.6e-17;
 Matches 98; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Oy 85 GGTGAAGCGGTAAGTGAAGTCTCCACTGTGAGGAGGGCTACCGATTGGAAAGCCA 144
Db 99 GGTGAAGTGTGAAGTGAAGTCTTCACTGTGAGGAGGGCTTCACTGTGAAGAGCC 158
Oy 145 AGTGAAGACCCCTGGACACGAGTCTTAAGTCTACCCAGGGTGCATAATCT 197
Db 159 AGTGAAGACCCCTGGACACGAGTCTTAAGTCTACCCAGGGTGCATAATCT 211

RESULT 13
CF222542
LOCUS CF222542 791 bp mRNA linear EST 04-AUG-2003
DEFINITION AGNCOURT 14926978 NICHG_XGC_Bmb5 Silurana tropicalis cDNA clone
IMAGE:6981334 5', mRNA sequence.
ACCESSION CF222542
VERSION CF222542.1 GI:33423250
KEYWORDS EST.
SOURCE Silurana tropicalis (western clawed frog)
ORGANISM Silurana tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipelidae; Pipidae;
Xenopodidae; Silurana.

1 (bases 1 to 791)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaapb@mail.nih.gov

Tissue Procurement: Robert M. Grainger
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14642 row: f column: 21
High quality sequence start: 3
High quality sequence stop: 755.
Location/Qualifiers

1..791
/organism="Silurana tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8164"
/clone="IMAGE:6981334"
/tissue_type="gastrula"
/dev_stage="embryo, stages 10-13"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHG_XGC_Bmb5"
/note="vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.0 kb. Constructed by Invitrogen. Note: This is a
Xenopus Gene Collection (XGC) library."

ORIGIN
Query Match 44.5%; Score 88.2; DB 14; Length 791;
Best Local Similarity 65.5%; Pred. No. 8.5e-17;
Matches 129; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Oy 1 TATGAAGCAGCGATGTTTACTTTTGAACATGATATCTCAGTTTCAACAGGACGCTT 60
Db 267 TACATGCTGCTCTTGAAGACCTTTTATCATGCTGCTTCAATTTGAAGAAACCTC 326
Oy 61 GCAAGAGCTGGATTATGCTTTAGGTGAAGCGATTAAGTCTTCCACTGTGGA 120
Db 327 GCTAAGCTGGATTATGCTTTAGGTGAAGCGATTAAGTCTTCCACTGTGGA 386
Oy 121 GCGAGGCTCAAGATGGAAGCAAGTGGACCCCTGGACACGAGTCTTAAGTCTACT 180
Db 387 GGAAGCTTAAATTTGCTGGGCAACAGATGCTTGGGAGAGAGTCCAGGCGAT 446

Oy 181 CCAGGGTGCAATACCT 197
Db 447 CCGAGTCAAGTCTCT 463

RESULT 14
BY662508
LOCUS BY662508 373 bp mRNA linear EST 16-DEC-2002
DEFINITION BY662508 RIKEN full-length enriched, 14.5 days embryo RP-
Ratke's pouches Mus musculus cDNA clone N720015L24 3', mRNA
sequence.

ACCESSION BY662508
VERSION BY662508.1 GI:27033688
KEYWORDS EST
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 373)

Okazaki, Y., Furuno, M., Kanukawa, T., Adachi, J., Hono, H., Kondo, S.,
Nikaido, I., Otsu, N., Saito, R., Suzuki, M., Yamana, I.,
Kiyosawa, M., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojohori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanpin, A., Matsuda, H.,
Batalov, S., Belski, R.W., Blake, J.A., Brade, D., Brasic, V.,
Chochia, C., Corbani, L.E., Cousins, S., Dalla, S., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Fraser, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanai, A.,
Kawai, H., Kawasawa, Y., Kedzierzki, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lanhard, B., Lyons, P.A., Maglott, D.R.,
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Numata, K., Okido, T., Pavan, W.J., Perles, G., Penole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Satou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Tansley, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wymshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M.,
Sakazawa, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, M., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shingawa, A., Yamashita, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,777 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
PUBMED
12466851

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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Kono, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, X., Numata, K.,
Ohno, M., Sakai, K., Sakazawa, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watanabe, M., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome. 43, 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Michelle Brinkmeier and Sally Camper (Dept.
Human Genetics University of Michigan Medical School 4301
MSRB 3 1500 W. Medical Center Dr. Ann Arbor, MI 48109-0618 USA)
whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

FEATURES
source Location/Qualifiers
1..373
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="N720015L24"
/tissue_type="Ratke's pouches"
/dev_stage="14.5 days embryo RP-"
/clone_lib="RIKEN full-length enriched, 14.5 days embryo
RP-"
Ratke's pouches"

ORIGIN
Query Match 43.0%; Score 87; DB 13; Length 373;
Best Local Similarity 94.4%; Pred. No. 1.4e-16;
Matches 101; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Oy 82 TTAGTGAAGCGATTAAGTGAAGTCTTCACTGTGAGGAGGGCTACCGATTGGAA 140
Db 113 TTAGTGAAGCGATTAAGTGAAGTCTTCACTGTGAGGAGGGCTACCGATTGGAA 172
Oy 141 GCAAGTGAAGACCCCTGGACACGAGTCTTAAGTCTACCCAGGCT 187
Db 173 GCAAGTGAAGACCCCTGGACACGAGTCTTAAGTCTACCCAGGCT 219

RESULT 15
BZ242580
LOCUS BZ242580 849 bp DNA linear GSS 12-OCT-2002
DEFINITION CH230-252D1.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-252D1, genomic survey sequence.

ACCESSION BZ242580
VERSION BZ242580.1 GI:23902844
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus

1 (bases 1 to 849)
Zhao, S., Shetty, J., Shatsman, S., Tseng, G., Gear, K.,
Shivabashyn, A., Greengard, R., Overton, L., Russell, D., Chen, D.,
Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Other GSS: CH230-252D1.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: shaying@igrr.org

Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@igrr.org).
Clones may be purchased from BACpac Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end

page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 252 row: D column: 1
Seq primer: T7
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..849
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/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCM"
/db_xref="taxon:10116"
/clone="CH230-252D1"
/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 rat (BN/SsNHsd/MCM) BAC library produced by
Pieter de Jong"

ORIGIN
Query Match 43.0%; Score 85.2; DB 20; Length 849;
Best Local Similarity 96.7%; Pred. No. 7.8e-16;
Matches 87; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 TATGAAGCAGCGATGTTTACTTTTGAACATGATATATCTCAGTTTCAACAGGAGCAGCTT 60
Db 197 TATGAAGCAGCGATGTTTACTTTTGAACATGATATATCTCAGTTTCAACAGGAGCAGCTT 256
Oy 61 GCAAGAGCTGGATTATGCTTTAGGTGAAGCGATTAAGTCTTCCACTGTGGA 120
Db 257 GCAAGAGCTGGATTATGCTTTAGGTGAAGCGATTAAGTCTTCCACTGTGGA 386

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